

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 14:14:49 ; Search time 24 Seconds
(without alignments)
21.554 Million cell updates/sec

Title: US-09-845-726a-1_COPY_2_12
Perfect score: 58
Sequence: 1 AHKSEVAHFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	609	1	ALBU_HUMAN
2	57	98.3	608	1	ALBU_RAT
3	54	93.1	600	1	ALBU_MACMU
4	54	93.1	609	1	ALBU_MERUN
5	53	91.4	607	1	ALBU_BOVIN
6	52	89.7	608	1	ALBU_RABIT
7	49	84.5	608	1	ALBU_MOUSE
8	48	82.8	607	1	ALBU_HORSE
9	48	82.8	607	1	ALBU_SHEEP
10	48	82.8	608	1	ALBU_FELCA
11	47	81.0	605	1	ALBU_PIG
12	45	77.6	615	1	ALBU_CHICK
13	44	75.9	40	1	ALBU_TRASC
14	43	74.1	608	1	ALBU_CANFA
15	37	63.8	1002	1	RBMC_MOUSE
16	36	62.1	719	1	FRE4_YEAST
17	35	60.3	155	1	R122_ARCFU
18	35	60.3	194	1	ITPA_HUMAN
19	35	60.3	324	1	CATV_NPVCD
20	35	60.3	1308	1	MAK6_MOUSE
21	35	60.3	1332	1	MAK6_HUMAN
22	34	58.6	200	1	HAM1_CAMJ2
23	34	58.6	478	1	Y143_MYCLE
24	34	58.6	488	1	Y1CJ_ECOLI
25	34	58.6	512	1	SYM_MYCPN
26	34	58.6	520	1	CLIA_BOVIN
27	34	58.6	520	1	CLIA_CAPHI
28	34	58.6	625	1	PKN1_THETN
29	34	58.6	685	1	PKN2_CLOPE
30	34	58.6	1121	1	DPOL_ADEGI
31	34	58.6	1597	1	RRL1_YEAST
32	33	56.9	185	1	VG16_HAEIN
33	33	56.9	219	1	YQFA_ECOLI

34	33	56.9	242	1	DJB3_MOUSE
35	33	56.9	247	1	YJ83_YEAST
36	33	56.9	316	1	LEG8_HUMAN
37	33	56.9	316	1	LEG8_MOUSE
38	33	56.9	316	1	LEG8_RAT
39	33	56.9	449	1	CL3A_MYCTU
40	33	56.9	498	1	PDI_RICCO
41	33	56.9	532	1	YKF3_CABEL
42	33	56.9	690	1	HYUA_PSEN
43	33	56.9	842	1	PLEC_CAUCR
44	33	56.9	919	1	ATC1_RAT
45	33	56.9	948	1	PMA5_ARATH

O35723	mus musculus
P47150	saccharomyc
O00214	homo sapien
O9j115	mus musculus
O62665	rattus norv
O08447	mycobacteri
O43116	ricinus com
P34266	caenorhabdi
O01262	pseudomonas
P37894	caulobacter
O64566	rattus norv
Q9s1b3	arabidopsis

ALIGNMENTS

RESULT 1
ALBU_HUMAN
ID ALBU_HUMAN STANDARD; PRT; 609 AA.
AC P02768; O95574; Q13140; Q9P157; Q9P117; Q9UHS3; Q9UJZ0;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196112; PubMed=3009475;
RA Minihetti P.P., Ruffner D.E., Kuang W.J., Dennison O.E., Hawkins J.W.,
RA Beattie W.G., Dugaiczky A.;
RT "Molecular structure of the human albumin gene is revealed by
RT nucleotide sequence within q11-22 of chromosome 4.";
RL J. Biol. Chem. 261:6747-6757(1986).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT LYS-420.
RX MEDLINE=82081982; PubMed=6171778;
RA Lawn R.M., Adelman J., Bock S.C., Franke A.E., Houck C.M.,
RA Najarian R.C., Seeburg P.H., Wion K.L.;
RT "The sequence of human serum albumin cDNA and its expression in E.
RT coli.";
RL Nucleic Acids Res. 9:6103-6114(1981).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT GLY-121.
RX MEDLINE=82105994; PubMed=6275391;
RA Dugaiczky A., Law S.W., Dennison O.E.;
RT "Nucleotide sequence and the encoded amino acids of human serum
RT albumin mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:71-75(1982).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Yang S., Zhang R.A., Qi Z.W., Yuan Z.Y.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (PRO0903/PRO1708/PRO2044/PRO2619/PRO2675).
RC TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,
RA Xu W., Gao F., Liu M., He F., Zhang Y., Ouyang S., Luo L.;
RT "Functional prediction of the coding sequences of 121 new genes
RT deduced by analysis of cDNA clones from human fetal liver.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A., AND VARIANT HIROSHIMA-1 LYS-378.
RA Huang M.C., Wu H.T.;
RT "The cDNA sequences of human serum albumin.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.

RC TISSUE=Liver, and Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Kirschner D.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE OF 25-609.
RX MEDLINE=76187907; PubMed=1225573;
RA Meloun B., Moravsek L., Kostka V.;
RT "Complete amino acid sequence of human serum albumin.";
RL FEBS Lett. 58:134-137(1975).
RN [9]
RP SEQUENCE OF 25-609.
RX Brown J.R., Shockley P., Behrens P.Q.;
RL (In) Bing D.H. (eds.);
RL The chemistry and physiology of the human plasma proteins, pp.23-40,
RL Pergamon Press, New York (1979).
RN [10]
RP SEQUENCE OF 1-455 FROM N.A.
RC TISSUE=Liver;
RA Menaya J., Parrilla R., Ayuso M.S.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE OF 1-26 FROM N.A.
RX MEDLINE=86140099; PubMed=2419329;
RA Urano Y., Watanabe K., Sakai M., Tamaoki T.;
RT "The human albumin gene. Characterization of the 5' and 3' flanking
RT regions and the polymorphic gene transcripts.";
RL J. Biol. Chem. 261:3244-3251(1986).
RN [12]
RP SEQUENCE OF 222-229.
RX MEDLINE=76257808; PubMed=955075;
RA Walker J.E.;
RT "Lysine residue 199 of human serum albumin is modified by
RT acetylsalicylic acid.";
RL FEBS Lett. 66:173-175(1976).
RN [13]
RP SEQUENCE OF 25-44 AND 480-499.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
RN [14]
RP DISULFIDE BONDS.
RA Sabar M.A., Stockbauer P., Moravsek L., Meloun B.;
RT "Disulfide bonds in human serum albumin.";
RL Collect. Czech. Chem. Commun. 42:564-579(1977).
RN [15]
RP BILIRUBIN-BINDING SITE.
RX MEDLINE=78186630; PubMed=656055;
RA Jacobsen C.;
RT "Lysine residue 240 of human serum albumin is involved in high-
RT affinity binding of bilirubin.";
RL Biochem. J. 171:453-459(1978).

RN RP VARIANTS TORINO LYS-84; VARESE HIS-23 AND VIBO VALENTIA LYS-106.
RX MEDLINE=91062352; PubMed=2247440;
RA Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J.,
RA Watkins S., Putnam F.W.;
RT "Mutations in genetic variants of human serum albumin found in
RT Italy.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8721-8725(1990).
RN [22]
RP VARIANT VENEZIA.
RX MEDLINE=91296740; PubMed=2068071;
RA Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M.,
RA Minchiotti L., Putnam F.W.;
RT "A donor splice mutation and a single-base deletion produce two
RT carboxyl-terminal variants of human serum albumin.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
RN [23]
RP VARIANTS IOWA CITY-2 VAL-25; IOWA CITY-1 VAL-389; KOMAGOME-3 HIS-23;
RX KOMAGOME-2 ARG-152 AND KOMAGOME-1 GLU-396.
RX MEDLINE=92052189; PubMed=1946412;
RA Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E.,
RA Matsuda Y.-I., Amaki I., Putnam F.W.;
RT "Genetic variants of serum albumin in Americans and Japanese.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
RN [24]
RP VARIANT CASEBROOK ASN-518.
RX MEDLINE=91316157; PubMed=1859851;
RA Peach R.J., Brennan S.O.;
RT "Structural characterization of a glycoprotein variant of human serum
RT albumin: albumin Casebrook (494 Asp-->Asn).";
RL Biochim. Biophys. Acta 1097:49-54(1991).
RN [25]
RP VARIANTS SONDRIO LYS-357 AND PARIS-2 ASN-587.
RX MEDLINE=92190239; PubMed=1347703;
RA Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
RA Rochu D., Porta F.;
RT "Two albumins with identical electrophoretic mobility are produced

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Query Match      100.0%; Score 58; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
DB 26 AHKSEVAHRFK 36
|||||
|

RESULT 2
ALBU_RAT
ID ALBU_RAT STANDARD; PRT; 608 AA.
AC P02770; P11382;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)].
GN ALB
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-81223722; PubMed-7017712;
RA Sargent T.D., Yang M., Bonner J.;
RT "Nucleotide sequence of cloned rat serum albumin messenger RNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:243-246(1981).
RN [2]
RP SEQUENCE OF 1-38, AND PROCESSING.
RX MEDLINE-77249657; PubMed-893447;
RA Strauss A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts A.W.;
RT "Rat liver pre-proalbumin: complete amino acid sequence of the pre-
piece. Analysis of the direct translation product of albumin
messenger RNA.";
RL J. Biol. Chem. 252:6846-6855(1977).
RN [3]
RP SEQUENCE OF 25-222.
RX MEDLINE-78109429; PubMed-564345;
RA Isemura S., Ikenaka T.;
RT "Amino acid sequences of fragments I and II obtained by cyanogen
bromide cleavage of rat serum albumin.";
RL J. Biochem. 83:35-48(1978).
RN [4]
RP SEQUENCE OF 223-288 AND 572-608.
RX MEDLINE-76260153; PubMed-956149;
RA Isemura S., Ikenaka T.;
RT "Fragmentation of rat serum albumin by cyanogen bromide cleavage and
the amino acid sequences of four fragments.";
RL J. Biochem. 79:1183-1196(1976).
RN [5]
RP SEQUENCE OF 166-174.
RX TISSUE-Plasma;
RN [6]
RP MEDLINE-87194805; PubMed-2437111;
RA Caraway R.E., Mitra S.P., Cochrane D.E.;
RT "Structure of a biologically active neurotensin-related peptide
obtained from pepsin-treated albumin(s).";
RL J. Biol. Chem. 262:5968-5973(1987).
RN [6]
RP COPPER-BINDING.
RX MEDLINE-79001617; PubMed-80265;
RA Aoyagi Y., Ikenaka T., Ichida F.;
RT "Copper(II)-binding ability of human alpha-fetoprotein.";
RL Cancer Res. 38:3483-3486(1978).
CC -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
hormones, bilirubin and drugs. Its main function is the regulation
of the colloidal osmotic pressure of blood.
CC -1- FUNCTION: NRP REGULATES FAT DIGESTION, LIPID ABSORPTION, AND
BLOOD FLOW (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.

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CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -1- SIMILARITY: Contains 3 albumin domains.
CC -----
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CC -----
CC EMBL: V01222; CAA24532.1; -.
DR PIR: A93872; ABRYS.
DR HSSP: P02768; 1E7B.
DR InterPro: IPR000264; Serum_albumin.
DR Pfam: PF00273; transport_prot; 3.
DR PRINTS: PR00802; SERUMALBUMIN.
DR ProDom: PD002486; Serum_albumin; 1.
DR SMART: SM00103; ALBUMIN; 3.
DR PROSITE: PS00212; ALBUMIN; 3.
KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 608
FT PEPTIDE 166 174
FT DOMAIN 25 205
FT DOMAIN 212 397
FT DOMAIN 404 595
FT METAL 27 27
FT DISULFID 77 86
FT DISULFID 99 115
FT DISULFID 114 125
FT DISULFID 148 193
FT DISULFID 192 201
FT DISULFID 224 270
FT DISULFID 269 277
FT DISULFID 289 303
FT DISULFID 302 313
FT DISULFID 340 385
FT DISULFID 384 393
FT DISULFID 416 462
FT DISULFID 461 472
FT DISULFID 485 501
FT DISULFID 500 511
FT DISULFID 538 583
FT DISULFID 582 591
FT VARIANT 262 262
FT CONFLICT 174 174
SQ SEQUENCE 608 AA; 68718 MW; 5BB497A282411AB7 CRC64;
Query Match      98.3%; Score 57; DB 1; Length 608;
Best Local Similarity 90.9%; Pred. No. 0.0022;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
DB 26 AHKSEVAHRFK 36
|||||
|

RESULT 3
ALBU_MACMU
ID ALBU_MACMU STANDARD; PRT; 600 AA.
AC Q28522;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Fragment).
GN ALB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;

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RN SEQUENCE FROM N.A.
RP MEDLINE-93211971; PubMed-8460152;
RA Watkins S.A., Sakamoto Y., Madison J.M., Davis E.M., Smith D.G.,
RT Wulet J., Putnam F.W.;
RA *CDNA and protein sequence of polymorphic macaque albumins that differ
RT in bilirubin binding.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2409-2413(1993).
CC -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -1- SIMILARITY: Contains 3 albumin domains.
CC -----
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CC -----
CC EMBL; M90463; AAA36906.1; -.
CC DR PIR; A47391; A47391.
CC DR HSP; P02768; IE7B.
CC DR InterPro; IPR000264; Serum_albumin.
CC DR Pfam; PF00273; transport_prot; 3.
CC DR PRINTS; PR00802; SERUMALBUMIN.
CC DR PRODOM; PD002486; Serum_albumin; 1.
CC DR SMART; SM00103; ALBUMIN; 3.
CC DR PROSITE; PS00212; ALBUMIN; 3.
CC DR Metal-binding; Lipid-binding; Repeat; Signal; Copper.
CC NON_TER 1 1
CC FT SIGNAL <1 10 BY SIMILARITY.
CC FT BINDING 11 16 BY SIMILARITY.
CC FT PROPEP 11 16 SERUM ALBUMIN.
CC FT CHAIN 17 600 ALBUMIN 1.
CC FT DOMAIN 17 197 ALBUMIN 1.
CC FT DOMAIN 204 389 ALBUMIN 2.
CC FT DOMAIN 396 587 ALBUMIN 3.
CC FT METAL 19 19 COPPER (BY SIMILARITY).
CC FT BINDING 256 256 BILIRUBIN (POTENTIAL).
CC FT DISULFID 69 78 BY SIMILARITY.
CC FT DISULFID 91 107 BY SIMILARITY.
CC FT DISULFID 106 117 BY SIMILARITY.
CC FT DISULFID 140 185 BY SIMILARITY.
CC FT DISULFID 184 193 BY SIMILARITY.
CC FT DISULFID 216 262 BY SIMILARITY.
CC FT DISULFID 261 269 BY SIMILARITY.
CC FT DISULFID 281 295 BY SIMILARITY.
CC FT DISULFID 294 305 BY SIMILARITY.
CC FT DISULFID 332 377 BY SIMILARITY.
CC FT DISULFID 376 385 BY SIMILARITY.
CC FT DISULFID 408 454 BY SIMILARITY.
CC FT DISULFID 453 464 BY SIMILARITY.
CC FT DISULFID 477 493 BY SIMILARITY.
CC FT DISULFID 492 503 BY SIMILARITY.
CC FT DISULFID 530 575 BY SIMILARITY.
CC FT DISULFID 574 583 BY SIMILARITY.
CC SEQUENCE 600 AA; 67880 MW; E45C871A670E740B CRC64;
Query Match 93.1%; Score 54; DB 1; Length 600;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 HKSEVAHRFK 11
| | | | | | | | | |
Db 19 HKSEVAHRFK 28
RESULT 4

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ALBU_MERUN STANDARD; PRT; 609 AA.
ID AC Q35030;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OC NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGS IDR; TISSUE=Liver;
RX MEDLINE-98116663; PubMed-9455485;
RA Yoshida K., Seto-Onshima A., Sinozara H.;
RT *Sequencing of cDNA encoding serum albumin and its extrahepatic
RL DNA Res. 4:351-354(1997).
CC -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -1- SIMILARITY: Contains 3 albumin domains.
CC -----
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CC -----
CC EMBL; AB006197; BAA21765.1; -.
CC DR PIR; JC5838; JC5838.
CC DR HSP; P02768; IE7B.
CC DR InterPro; IPR000264; Serum_albumin.
CC DR Pfam; PF00273; transport_prot; 3.
CC DR PRINTS; PR00802; SERUMALBUMIN.
CC DR PRODOM; PD002486; Serum_albumin; 1.
CC DR SMART; SM00103; ALBUMIN; 3.
CC DR PROSITE; PS00212; ALBUMIN; 3.
CC DR Metal-binding; Lipid-binding; Repeat; Signal; Copper.
CC FT SIGNAL 1 18 BY SIMILARITY.
CC FT PROPEP 19 24 BY SIMILARITY.
CC FT CHAIN 25 609 SERUM ALBUMIN.
CC FT DOMAIN 25 206 ALBUMIN 1.
CC FT DOMAIN 213 398 ALBUMIN 2.
CC FT DOMAIN 405 596 ALBUMIN 3.
CC FT METAL 28 28 COPPER.
CC FT DISULFID 78 87 BY SIMILARITY.
CC FT DISULFID 100 116 BY SIMILARITY.
CC FT DISULFID 115 126 BY SIMILARITY.
CC FT DISULFID 149 194 BY SIMILARITY.
CC FT DISULFID 193 202 BY SIMILARITY.
CC FT DISULFID 225 271 BY SIMILARITY.
CC FT DISULFID 270 278 BY SIMILARITY.
CC FT DISULFID 290 304 BY SIMILARITY.
CC FT DISULFID 303 314 BY SIMILARITY.
CC FT DISULFID 341 386 BY SIMILARITY.
CC FT DISULFID 385 394 BY SIMILARITY.
CC FT DISULFID 417 463 BY SIMILARITY.
CC FT DISULFID 462 473 BY SIMILARITY.
CC FT DISULFID 486 502 BY SIMILARITY.
CC FT DISULFID 501 512 BY SIMILARITY.
CC FT DISULFID 539 584 BY SIMILARITY.
CC FT DISULFID 583 592 BY SIMILARITY.
CC SEQUENCE 609 AA; 68940 MW; 9CA5F97F67E1A48 CRC64;
SQ

```

Query Match 93.1%; Score 54; DB 1; Length 609;
 Best Local Similarity 81.8%; Pred. No. 0.0082;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
 |||||:||||:
 Db 27 AHKSEIAHRYK 37

RESULT 5

ALBU_BOVIN STANDARD; PRT: 607 AA.
 AC P02769; Q02787;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serum albumin precursor (Allergen Bos d 6).
 GN ALB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RN [2]
 RN [3]
 RA Holowachuk E.W., Stoltenborg J.K., Reed R.G., Peters T. Jr.;
 RL Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT THR-214.
 RC TISSUE=Liver;
 RA Barry T., Power S., Gannon F.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Hilger C., Grigioni F., de Beaufort C., Michel G., Hentges F.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANT THR-214.
 RA Wu H.T., Huang M.C.;
 RL "The complete cDNA sequence of bovine serum albumin.";
 RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1-32.
 RX MEDLINE=80024278; PubMed=488109;
 RA McGilivray R.T.A., Chung D.W., Davie E.W.;
 RT "Biosynthesis of bovine plasma proteins in a cell-free system. Amino-terminal sequence of preproalbumin.";
 RL Eur. J. Biochem. 98:477-485(1979).
 RN [6]
 RP SEQUENCE OF 25-424 AND 429-607, AND VARIANT THR-214.
 RA Brown J.R.;
 RL "Structure of bovine serum albumin.";
 RT Fed. Proc. 34:591-591(1975).
 RN [7]
 RP REVISIONS TO 190-195.
 RA Brown J.R.;
 RL Submitted (APR-1975) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 402-433.
 RX MEDLINE=82023364; PubMed=7283978;
 RA Reed R.G., Putnam F.W., Peters T. Jr.;
 RL "Sequence of residues 400-403 of bovine serum albumin.";
 RT Biochem. J. 191:867-868(1980).
 RN [9]
 RP SEQUENCE OF 19-28.
 RX MEDLINE=77134075; PubMed=843354;
 RA Patterson J.E., Geller D.M.;
 RT "Bovine microsomal albumin: amino terminal sequence of bovine proalbumin.";
 RL Biochem. Biophys. Res. Commun. 74:1220-1226(1977).
 RN [10]

RP SEQUENCE, AND REVISIONS TO 118-119 AND 180.
 RX MEDLINE=91083649; PubMed=2260975;
 RA Hirayama K., Akashi S., Furuya M., Fukuhara K.-I.;
 RT "Rapid confirmation and revision of the primary structure of bovine serum albumin by ESIMS and Frit-FAB LC/MS.";
 RL Biochem. Biophys. Res. Commun. 173:639-646(1990).
 RN [11]
 RP SEQUENCE OF 25-41.
 RX MEDLINE=88267456; PubMed=3389500;
 RA Hsieh J.C., Lin F.P., Tam M.F.;
 RT "Electroblotting onto glass-fiber filter from an analytical isoelectrofocusing gel: a preparative method for isolating proteins for N-terminal microsequencing.";
 RL Anal. Biochem. 170:1-8(1988).
 RN [12]
 RP SEQUENCE OF 437-451.
 RA Vilbois F.;
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.
 RN [13]
 RP DISULFIDE BONDS.
 RA Brown J.R.;
 RL "Structure of serum albumin: disulfide bridges.";
 RT Fed. Proc. 33:1389-1389(1974)
 CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
 CC -!- SIMILARITY: Contains 3 albumin domains.
 CC -----
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 CC -----
 DR EMBL; M73993; AAA51411.1;
 DR EMBL; X58989; CAA41735.1;
 DR EMBL; Y17769; CAA76847.1;
 DR EMBL; AF542068; AAN17824.1;
 DR HSSP; P02768; 1E7B.
 DR InterPro; IPR00264; Serum albumin.
 DR Pfam; PF00273; transport_prot; 3.
 DR PRINTS; PR00802; SERUMALBUMIN.
 DR ProDom; PD002486; Serum_albumin; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 KW Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen;
 KW Polymorphism.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 607 SERUM ALBUMIN.
 FT DOMAIN 25 204 ALBUMIN 1.
 FT DOMAIN 211 396 ALBUMIN 2.
 FT DOMAIN 403 594 ALBUMIN 3.
 FT METAL 27 27 COPPER (BY SIMILARITY).
 FT DISULFID 77 86
 FT DISULFID 99 115
 FT DISULFID 114 125
 FT DISULFID 147 192
 FT DISULFID 191 200
 FT DISULFID 223 269
 FT DISULFID 268 276
 FT DISULFID 288 302
 FT DISULFID 301 312
 FT DISULFID 339 384
 FT DISULFID 383 392
 FT DISULFID 415 461
 FT DISULFID 460 471

FT DISULFID 484 500
 FT DISULFID 499 510
 FT DISULFID 537 582
 FT DISULFID 581 590
 FT VARIANT 214 214
 FT CONFLICT 302 302
 FT CONFLICT 304 305
 FT CONFLICT 324 324
 FT CONFLICT 394 395
 FT CONFLICT 437 437
 FT CONFLICT 493 494
 SQ SEQUENCE 607 AA; 69293 MW; 39167DFE76858D4 CRC64;

Query Match 91.4%; Score 53; DB 1; Length 607;
 Best Local Similarity 90.0%; Pred. No. 0.013; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0;

QY 2 HKSEVAHRFK 11
 DB 27 HKSEIAHRFK 36
 |||||:|||||

RESULT 6
 ALBU_RABIT STANDARD; PRT; 608 AA.
 AC P49065;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serum albumin precursor.
 GN ALB.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Liver;
 RA Sheffield W.P., Syed S., Schuyler P.D.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
 binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
 hormones, bilirubin and drugs. Its main function is the regulation
 of the colloidal osmotic pressure of blood.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
 CC -!- SIMILARITY: Contains 3 albumin domains.

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 or send an email to license@sib-sib.ch).
 CC -----

DR EMBL: U18344; AAB58347.1; -.
 DR HSP: P02768; IEB7.
 DR InterPro: IPR000264; Serum_albumin.
 DR Pfam: PF00273; transport_prot; 3.
 DR PRINTS: PR00802; SERUMALBUMIN.
 DR ProDom: PD002486; Serum_albumin; 1.
 DR SMART: SM00103; ALBUMIN; 3.
 DR PROSITE: PS00212; ALBUMIN; 3.
 KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 608 BY SIMILARITY.
 FT DOMAIN 25 205 SERUM ALBUMIN.
 FT DOMAIN 212 397 ALBUMIN 1.
 FT DOMAIN 404 595 ALBUMIN 2.
 FT DOMAIN 404 595 ALBUMIN 3.
 FT METAL 27 27 COPPER.

FT DISULFID 77 86 BY SIMILARITY.
 FT DISULFID 99 115 BY SIMILARITY.
 FT DISULFID 114 125 BY SIMILARITY.
 FT DISULFID 148 193 BY SIMILARITY.
 FT DISULFID 192 201 BY SIMILARITY.
 FT DISULFID 224 270 BY SIMILARITY.
 FT DISULFID 269 277 BY SIMILARITY.
 FT DISULFID 289 303 BY SIMILARITY.
 FT DISULFID 302 313 BY SIMILARITY.
 FT DISULFID 340 385 BY SIMILARITY.
 FT DISULFID 384 393 BY SIMILARITY.
 FT DISULFID 416 461 BY SIMILARITY.
 FT DISULFID 461 472 BY SIMILARITY.
 FT DISULFID 485 501 BY SIMILARITY.
 FT DISULFID 500 511 BY SIMILARITY.
 FT DISULFID 538 583 BY SIMILARITY.
 FT DISULFID 582 591 BY SIMILARITY.
 SQ SEQUENCE 608 AA; 68914 MW; CF5E92647AAFE9A2 CRC64;

Query Match 89.7%; Score 52; DB 1; Length 608;
 Best Local Similarity 90.0%; Pred. No. 0.02;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRF 10
 DB 26 AHKSEIAHRF 35
 |||||:|||||

RESULT 7
 ALBU_MOUSE STANDARD; PRT; 608 AA.
 ID ALBU_MOUSE
 AC P07724; Q61802;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serum albumin precursor.
 GN ALB OR ALB1 OR ALB-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA van Reeth T., Gabant P., Dreze P., Szpirer J., Szpirer C.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE OF 99-516 FROM N.A.
 RX MEDLINE=88216123; PubMed=2452956;

RA Minghetti P.P., Law S.W., Dugaiczak A.;
 RT "The rate of molecular evolution of alpha-fetoprotein approaches that
 of pseudogenes.";
 RL Mol. Biol. Evol. 2:347-358(1985).
 RN [4]
 RP SEQUENCE OF 477-551 FROM N.A.
 RC STRALINE-BALB/C;
 RX MEDLINE=90269606; PubMed=1971802;
 RA Boccaccio C., Deschattre J., Meunier-Rotival M.;
 RT "Empty and occupied insertion site of the truncated LINE-1 repeat
 located in the mouse serum albumin-encoding gene.";
 RL Gene 88:181-186(1990).
 RN [5]
 RP SEQUENCE OF 25-44.
 RC TISSUE=Liver;
 RX MEDLINE=93162044; PubMed=1286668;
 RA Giometti C.S., Taylor J., Tollaksen S.L.;
 RT "Mouse liver protein database: a catalog of proteins detected by two-
 dimensional gel electrophoresis.";
 RL Electrophoresis 13:970-991(1992).
 CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
 binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
 hormones, bilirubin and drugs. Its main function is the regulation
 of the colloidal osmotic pressure of blood.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 CC -!- SIMILARITY: Contains 3 albumin domains.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; A011413; CAA03617.1; -;
 DR EMBL; M16111; AAA37190.1; -;
 DR EMBL; X13060; CAA31458.1; -;
 DR EMBL; AK010025; BAB26650.1; -;
 DR PIR; A05139; A05139.
 DR HSSP; P02768; LE7B.
 DR SWISS-2DPAGE; P07724; MOUSE.
 DR MGD; MGI:87991; Alb1.
 DR InterPro; IPR000264; Serum_albumin.
 DR Pfam; PF00273; transport_prot; 3.
 DR PRINTS; PR00802; SERUMALBUMIN.
 DR ProDom; PD002486; Serum_albumin; 1.
 DR SMART; SM00103; Albumin; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT PROPEP 19 24
 FT CHAIN 25 608
 FT DOMAIN 25 205 SERUM ALBUMIN.
 FT DOMAIN 212 397 ALBUMIN 1.
 FT DOMAIN 404 595 ALBUMIN 2.
 FT METAL 27 27 ALBUMIN 3.
 FT METAL 27 27 COPPER.
 FT DISULFID 77 86 BY SIMILARITY.
 FT DISULFID 99 115 BY SIMILARITY.
 FT DISULFID 114 125 BY SIMILARITY.
 FT DISULFID 148 193 BY SIMILARITY.
 FT DISULFID 192 201 BY SIMILARITY.
 FT DISULFID 224 270 BY SIMILARITY.
 FT DISULFID 269 277 BY SIMILARITY.
 FT DISULFID 289 303 BY SIMILARITY.
 FT DISULFID 302 313 BY SIMILARITY.
 FT DISULFID 340 385 BY SIMILARITY.
 FT DISULFID 384 393 BY SIMILARITY.
 FT DISULFID 416 462 BY SIMILARITY.
 FT DISULFID 461 472 BY SIMILARITY.
 FT DISULFID 485 501 BY SIMILARITY.

FT DISULFID 500 511 BY SIMILARITY.
 FT DISULFID 538 583 BY SIMILARITY.
 FT DISULFID 582 591 BY SIMILARITY.
 FT CONFLICT 27 27 H -> D (IN REF. 5).
 FT CONFLICT 33 33 H -> D (IN REF. 5).
 FT CONFLICT 41 41 Q -> I (IN REF. 5).
 SQ SEQUENCE 608 AA; 68692 MW; 292F7C7EED3A61B4 CRC64;
 Query Match 84.5%; Score 49; DB 1; Length 608;
 Best Local Similarity 80.0%; Pred. No. 0.075;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AHKSEVAHRP 10
 DB 26 AHKSEIAHRY 35
 RESULT 8
 ALBU_HORSE STANDARD; PRT; 607 AA.
 AC P35747;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serum albumin precursor.
 GN ALB.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_Taxid=9796;
 RN [1]
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RC TISSUE=Liver;
 RX MEDLINE=93345495; PubMed=8344282;
 RA Ho J.X., Holowachuk E.W., Norton E.J., Twigg P.D., Carter D.C.;
 RT "X-ray and primary structure of horse serum albumin (Equus caballus)
 at 0.27-nm resolution.";
 RL Eur. J. Biochem. 215:205-212(1993).
 CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
 binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
 hormones, bilirubin and drugs. Its main function is the regulation
 of the colloidal osmotic pressure of blood.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 CC -!- SIMILARITY: Contains 3 albumin domains.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X74045; CAA52194.1; -;
 DR PIR; S34053; ABHOS.
 DR HSSP; P02768; LE7B.
 DR InterPro; IPR000264; Serum_albumin.
 DR Pfam; PF00273; transport_prot; 3.
 DR PRINTS; PR00802; SERUMALBUMIN.
 DR ProDom; PD002486; Serum_albumin; 1.
 DR SMART; SM00103; Albumin; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT PROPEP 19 24
 FT CHAIN 25 607 SERUM ALBUMIN.
 FT DOMAIN 25 607
 FT DOMAIN 25 204 ALBUMIN 1.
 FT DOMAIN 211 396 ALBUMIN 2.
 FT METAL 27 27 ALBUMIN 3.
 FT DISULFID 77 86 COPPER (BY SIMILARITY).

1


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DR EMBL: X84842; CAA59279.1; -.
DR PIR: JC4660; S57632.
DR HSP: P02768; IE7B.
DR InterPro: IPR000264; Serum_albumin.
DR Pfam: PF00273; transport_prot; 3.
DR PRINTS: PR00802; SERUMALBUMIN.
DR ProDom: PD002486; Serum_albumin; 1.
DR SMART: SM00103; ALBUMIN; 3.
DR PROSITE: PS00212; ALBUMIN; 3.
KW Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 608
FT DOMAIN 23 205
FT DOMAIN 212 397
FT DOMAIN 404 595
FT METAL 27 27
FT DISULFID 77 86
FT DISULFID 99 115
FT DISULFID 114 125
FT DISULFID 148 193
FT DISULFID 192 201
FT DISULFID 224 270
FT DISULFID 269 277
FT DISULFID 289 303
FT DISULFID 302 333
FT DISULFID 340 385
FT DISULFID 384 393
FT DISULFID 416 462
FT DISULFID 461 472
FT DISULFID 485 501
FT DISULFID 500 511
FT DISULFID 535 583
FT DISULFID 582 591
SQ SEQUENCE 608 AA; 68659 MW; 07E629CAC5F60E5F CRC64;

Query Match 82.8%; Score 48; DB 1; Length 608;
Best Local Similarity 80.0%; Pred. No. 0.12;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRF 10
Db 26 AHQSEIAHRF 35
:::|||||

RESULT 11
ALBU_PIG STANDARD; PRT; 605 AA.
AC P08335; Q29018;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Fragment).
GN ALB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016582; PubMed=3174440;
RA Baldwin G.S.; Weinstock J.;
RT "Nucleotide sequence of porcine liver albumin.";
RL Nucleic Acids Res. 16:9045-9045(1988).
CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -!- SIMILARITY: Contains 3 albumin domains.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X12422; CAA30970.1; -.
DR EMBL: M36787; AAA30988.1; -.
DR PIR: S01382; AEPGS.
DR HSP: P02768; IE7H.
DR InterPro: IPR000264; Serum_albumin.
DR Pfam: PF00273; transport_prot; 3.
DR PRINTS: PR00802; SERUMALBUMIN.
DR ProDom: PD002486; Serum_albumin; 1.
DR SMART: SM00103; ALBUMIN; 3.
DR PROSITE: PS00212; ALBUMIN; 3.
KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
FT SIGNAL 1 16
FT PROPEP 17 22
FT CHAIN 23 605
FT DOMAIN 23 202
FT DOMAIN 209 394
FT DOMAIN 401 592
FT METAL 31 31
FT DISULFID 75 84
FT DISULFID 97 113
FT DISULFID 112 123
FT DISULFID 145 190
FT DISULFID 189 198
FT DISULFID 221 267
FT DISULFID 266 274
FT DISULFID 286 300
FT DISULFID 299 310
FT DISULFID 337 382
FT DISULFID 381 390
FT DISULFID 413 459
FT DISULFID 458 469
FT DISULFID 482 498
FT DISULFID 497 508
FT DISULFID 535 580
FT DISULFID 579 588
FT CONFLICT 562 562
SQ SEQUENCE 605 AA; 69410 MW; 3E536B0DD1A1F4FF CRC64;

Query Match 81.0%; Score 47; DB 1; Length 605;
Best Local Similarity 80.0%; Pred. No. 0.18;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRFK 11
Db 25 YKSEIAHRFK 34
:::|||||

RESULT 12
ALBU_CHICK STANDARD; PRT; 615 AA.
AC P19121;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Liver;
RA Cassidy A.I., Salkild C.K., Baverstock P., Wallace J.C.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE=83161037; PubMed=6187737;
RA Hache R.J.G., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deeley R.G.;
RT "The 5' noncoding and flanking regions of the avian very low density
RT apolipoprotein II and serum albumin genes. Homologies with the egg
RT white protein genes.;"
RL J. Biol. Chem. 258:4556-4564(1983).
RN [3]
RP SEQUENCE OF 19-30.
RX MEDLINE=78019943; PubMed=911327;
RA Rosen A.M., Geller D.M.;
RT "Chicken microsomal albumin: amino terminal sequence of chicken
RT proalbumin.;"
RL Biochem. Biophys. Res. Commun. 78:1060-1066(1977).
CC -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -1- SIMILARITY: Contains 3 albumin domains.
CC -----
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CC -----
DR EMBL; X60688; CAA43098.1; -.
DR EMBL; V00381; CAA23680.1; -.
DR PIR; S15571; ABCHS.
DR HSP; P02768; IE7B.
DR InterPro; IPR000264; Serum_albumin.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
FT SIGNAL 1 18
FT PROPEP 19 23
FT CHAIN 24 615 SERUM ALBUMIN.
FT DOMAIN 24 209 ALBUMIN 1.
FT DOMAIN 216 401 ALBUMIN 2.
FT DOMAIN 408 599 ALBUMIN 3.
FT METAL 30 30 COPPER (BY SIMILARITY).
FT DISULFID 80 89 BY SIMILARITY.
FT DISULFID 102 118 BY SIMILARITY.
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 152 197 BY SIMILARITY.
FT DISULFID 196 205 BY SIMILARITY.
FT DISULFID 228 274 BY SIMILARITY.
FT DISULFID 273 281 BY SIMILARITY.
FT DISULFID 293 307 BY SIMILARITY.
FT DISULFID 306 317 BY SIMILARITY.
FT DISULFID 344 389 BY SIMILARITY.
FT DISULFID 388 397 BY SIMILARITY.
FT DISULFID 420 466 BY SIMILARITY.
FT DISULFID 465 476 BY SIMILARITY.
FT DISULFID 489 505 BY SIMILARITY.
FT DISULFID 504 515 BY SIMILARITY.
FT DISULFID 542 587 BY SIMILARITY.
FT DISULFID 586 595 BY SIMILARITY.
FT CARBOHYD 500 500 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 24 20 F -> M (IN REF. 3).
SQ SEQUENCE 615 AA; 69918 MW; E59E4BBAC066C6 CRC64;

Query Match 77.6%; Score 45; DB 1; Length 615;
Best Local Similarity 77.8%; Pred. No. 0.45;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
DB 30 HKSEIAHRY 38
|||||:

RESULT 13
ALBU_TRASC STANDARD; PRT; 40 AA.
ID ALBU_TRASC
AC P81188;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 67 kDa serum albumin (Alb-1) (Fragment).
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.
OX NCBI_TaxID=34903;
RN [1]
RP SEQUENCE.
RX MEDLINE=98103404; PubMed=9440230;
RA Brown M.A., Chambers G.K., Licht P.;
RT "Purification and partial amino acid sequences of two distinct
RT albumins from turtle plasma.;"
RL Comp. Biochem. Physiol. 118B:367-374(1997).
RN [2]
RP SEQUENCE OF 1-8.
RX MEDLINE=95309661; PubMed=7789749;
RA Selcer K.W., Palmer B.D.;
RT "Estrogen downregulation of albumin and a 170-kDa serum protein in
RT the turtle, Trachemys scripta.;"
RL Gen. Comp. Endocrinol. 97:340-352(1995).
CC -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- MISCELLANEOUS: IN THE RED-EARED SLIDER TURTLE, THERE ARE TWO FORMS
CC OF ALBUMIN, ALB-1 AND ALB-2.
CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC HSP; P02768; IE7B.
CC InterPro; IPR000264; Serum_albumin.
CC Pfam; PF00273; transport_prot; 1.
CC PROSITE; PS00212; ALBUMIN; PARTIAL.
KW Metal-binding; Lipid-binding; Copper.
FT METAL 4 4 COPPER (BY SIMILARITY).
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4682 MW; 5FAC9E49E2789BB0 CRC64;

Query Match 75.9%; Score 44; DB 1; Length 40;
Best Local Similarity 77.8%; Pred. No. 0.037;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
DB 4 HKSEIVHRF 12
|||||:

RESULT 14
ALBU_CANFA STANDARD; PRT; 608 AA.
ID ALBU_CANFA
AC P49822; 077705; Q9TSZ4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Allergen Can f 3).
GN ALB.
OS Canis familiaris (Dog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Beagle; TISSUE=Liver;
 RA Hilger C.; Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=20148667; PubMed=10669848;
 RA Pandjaitan B., Swoboda I., Brandesky-Pichler F., Rumpold H.,
 RA Valenta R., Spitzauer S.;
 RT "Escherichia coli expression and purification of recombinant dog
 RT albumin, a cross-reactive animal allergen.";
 RL J. Allergy Clin. Immunol. 105:279-285(2000).
 RN [3]
 RN SEQUENCE OF 25-48.
 RP MEDLINE=75011422; PubMed=4414013;
 RX Dixon J.W., Sarkar B.;
 RA "Isolation, amino acid sequence and copper(II)-binding properties of
 RT peptide (1-24) of dog serum albumin.";
 RL J. Biol. Chem. 249:5872-5877(1974).
 RN [4]
 RN SEQUENCE OF 25-38.
 RP TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RL dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 RN [5]
 RN SEQUENCE OF 215-478 FROM N.A.
 RP TISSUE=Salivary gland;
 RX MEDLINE=94201492; PubMed=7512102;
 RA Spitzauer S., Schweiger C., Sperr W.R., Pandjaitan B., Valent P.,
 RA Muehl S., Ebner C., Scheiner O., Kraft D., Rumpold H.;
 RT "Molecular characterization of dog albumin as a cross-reactive
 RT allergen.";
 RL J. Allergy Clin. Immunol. 93:614-627(1994).
 CC -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
 CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
 CC hormones, bilirubin and drugs. Its main function is the regulation
 CC of the colloidal osmotic pressure of blood.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 albumin domains.
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 CC -----
 DR EMBL; AJ133489; CAB64867.1; -;
 DR EMBL; Y17737; CAA76841.1; -;
 DR EMBL; S72946; AAB30434.1; -;
 DR HSP; P02768; 1E7B.
 DR HSC-2DPAGE; P49822; DOG.
 DR InterPro; IPR000264; Serum_albumin.
 DR Pfam; PF00273; transprot_prot; 3.
 DR PRINTS; PR00802; SERUMALBUMIN.
 DR ProDom; PD002486; Serum_albumin; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 KW Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 24
 FT CHAIN 25 608 SERUM ALBUMIN.

FT	DOMAIN	25	205	ALBUMIN 1.
FT	DOMAIN	212	397	ALBUMIN 2.
FT	DOMAIN	404	595	ALBUMIN 3.
FT	METAL	27	27	COPPER (BY SIMILARITY).
FT	DISULFID	77	86	BY SIMILARITY.
FT	DISULFID	99	115	BY SIMILARITY.
FT	DISULFID	114	125	BY SIMILARITY.
FT	DISULFID	148	193	BY SIMILARITY.
FT	DISULFID	192	201	BY SIMILARITY.
FT	DISULFID	224	270	BY SIMILARITY.
FT	DISULFID	269	277	BY SIMILARITY.
FT	DISULFID	289	303	BY SIMILARITY.
FT	DISULFID	302	313	BY SIMILARITY.
FT	DISULFID	340	385	BY SIMILARITY.
FT	DISULFID	384	393	BY SIMILARITY.
FT	DISULFID	416	462	BY SIMILARITY.
FT	DISULFID	461	472	BY SIMILARITY.
FT	DISULFID	485	501	BY SIMILARITY.
FT	DISULFID	500	511	BY SIMILARITY.
FT	DISULFID	538	583	BY SIMILARITY.
FT	DISULFID	582	591	BY SIMILARITY.
FT	CONFLICT	1	26	MEWVFISLFLESSAYSRLVREA -> MDT (IN REF. 2).
FT	CONFLICT	146	146	A -> R (IN REF. 2).
FT	CONFLICT	206	206	I -> T (IN REF. 2).
FT	CONFLICT	349	349	V -> A (IN REF. 2).
FT	CONFLICT	359	359	S -> A (IN REF. 1).
FT	CONFLICT	448	448	V -> VV (IN REF. 5).
FT	CONFLICT	474	474	D -> E (IN REF. 1).
SQ	SEQUENCE	608 AA;	68606 MW;	3CFIC8FF7DD8FC06 CRC64;

Query Match 74.1%; Score 43; DB 1; Length 608;
 Best Local Similarity 70.0%; Pred. No. 1.1;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY	1	AHKSEVAHRF	10
Db	26	AYKSEIAHRY	35

RESULT 15
 RBMC_MOUSE STANDARD; PRT; 1002 AA.
 AC Q8R4X3; Q8R373; Q8R302; Q9CS80;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE RNA-binding protein 12 (RNA binding motif protein 12) (SH3/WW domain
 DE anchor protein in the nucleus) (SWAN).
 GN RBM12.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Huang C.-H.;
 RT "Identification of SWAN as a novel hnRNP-like adaptor protein with
 RT multiple domains and broadly expressed in mammalian tissues.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo, and Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	58	100.0	21	11	Q9QVA1		Q9qval rattus sp.
2	58	100.0	396	4	Q8IUK7		Q8iuk7 homo sapien
3	57	98.3	20	11	Q9QUX8		Q9qux8 rattus sp.
4	57	98.3	608	5	Q95VB7		Q95vb7 scytosoma
5	53	91.4	20	2	Q9R4X7		Q9r4x7 mycobacteri
6	52	89.7	40	6	Q9TRA5		Q9tra5 oryctolagus
7	49	84.5	205	11	Q8CGY4		Q8cgy4 mus musculus
8	49	84.5	608	11	Q8C7H3		Q8c7h3 mus musculus
9	45	77.6	30	13	Q9PRW0		Q9prw0 struthio ca
10	43	74.1	17	6	Q8TR98		Q8tr98 canis fami
11	43	74.1	20	6	Q8TQ26		Q8tq26 macaca fasc
12	39.5	68.1	201	16	Q9PQK4		Q9pqk4 ureaplasma
13	38	65.5	152	16	Q8EQM2		Q8eqm2 oceanobacill
14	38	65.5	3209	5	Q8I5D0		Q8i5d0 plasmodium
15	37	63.8	93	16	Q8YNI1		Q8yni1 anabaena sp
16	37	63.8	253	16	Q98NT8		Q98nt8 rhizobium l

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DE Similar to serum albumin precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035969; AAH35969.1; -.
SQ SEQUENCE 396 AA; 45159 MW; 756519C096463A9B CRC64;

Query Match 100.0%; Score 58; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
DB 26 AHKSEVAHREFK 36
|||||:|||||

RESULT 3
Q9QX8 PRELIMINARY; PRT; 20 AA.
AC Q9QX8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 70 kDa seizure activity-linked albumin-like glycoprotein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=96087830; PubMed=8587647;
RA Onozuka M., Imai S., Isobe T., Yen C.T., Watanabe K.;
FT "Purification and characterization of a novel 70-kDa brain protein
associated with seizure activities.";
RL Neurochem. Res. 20:901-905(1995).
DR HSP; P02768; IE7H.
SQ SEQUENCE 20 AA; 2381 MW; 534A23C0F9F70F7D CRC64;

Query Match 98.3%; Score 57; DB 11; Length 20;
Best Local Similarity 90.9%; Pred. No. 0.00015;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
DB 2 AHKSEIAHREFK 12
|||||:|||||

RESULT 4
Q95VB7 PRELIMINARY; PRT; 608 AA.
AC Q95VB7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Albumin.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RA Osman A., Asahi H., Stadecker M.J., LoVerde P.T.;
RT "Albumin precursor homolog is a novel T helper cell immunogenic egg
component in murine infection with Schistosoma mansoni.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF418550; AAL08579.1; -.
DR InterPro; IPR000264; Serum_albumin.

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DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PD00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 2.
SQ SEQUENCE 608 AA; 68225 MW; E5EABB28E1C66E54 CRC64;

Query Match 98.3%; Score 57; DB 5; Length 608;
Best Local Similarity 90.9%; Pred. No. 0.0071;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
DB 26 AHKSEIAHREFK 36
|||||:|||||

RESULT 5
Q9R4X7 PRELIMINARY; PRT; 20 AA.
AC Q9R4X7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 66 kDa SEROREACTIVE protein/serum albumin homolog (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RX MEDLINE=94343500; PubMed=8064836;
RA Deshpande R.G., Khan M.B., Bhat D.A., Navalkar R.G.;
FT "Purification and partial characterisation of a novel 66-kDa
seroreactive protein of Mycobacterium tuberculosis H37Rv.";
RL J. Med. Microbiol. 41:173-178(1994).
SQ SEQUENCE 20 AA; 2393 MW; 534A232072870F7D CRC64;

Query Match 91.4%; Score 53; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. No. 0.00098;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHREFK 11
DB 3 HKSEIAHREFK 12
|||||:|||||

RESULT 6
Q9TRA5 PRELIMINARY; PRT; 40 AA.
AC Q9TRA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Antagonist protein (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=94359514; PubMed=8078511;
RA Xu A., Narayanan N.;
FT "Purification, amino-terminal sequence and functional properties of a
64 kDa cytosolic protein from heart muscle capable of modulating
calcium transport across the sarcoplasmic reticulum in vitro.";
RL Mol. Cell. Biochem. 132:7-14(1994).
DR HSP; P02768; IE7H.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 1.
SQ SEQUENCE 40 AA; 4694 MW; BA7E0B69C6CE858C CRC64;

Query Match 89.7%; Score 52; DB 6; Length 40;
Best Local Similarity 90.0%; Pred. No. 0.0034;

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Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRF 10
 |||||:||||
 Db 2 AHKSEIAHRF 11

RESULT 7

Q8CG74 Q8CG74 PRELIMINARY; PRT; 205 AA.
 AC Q8CG74;
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Albumin (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvetACfBr;
 RA Van Reeth T., Dreze P.L., Gabant P., Szpirer C., Szpirer J.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ277794; CAC81903.1;
 FT NON_TER 205 205
 SQ SEQUENCE 205 AA; 23624 MW; 0A982E85C7474BF9 CRC64;

Query Match 84.5%; Score 49; DB 11; Length 205;
 Best Local Similarity 80.0%; Pred. No. 0.084;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRF 10
 |||||:||||
 Db 26 AHKSEIAHRF 35

RESULT 8

Q8C7H3 Q8C7H3 PRELIMINARY; PRT; 608 AA.
 AC Q8C7H3;
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Albumin I.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL: AK050248; BAC34145.1; --
 SQ SEQUENCE 608 AA; 68722 MW; 292F600EED3A61B4 CRC64;

Query Match 84.5%; Score 49; DB 11; Length 608;
 Best Local Similarity 80.0%; Pred. No. 0.28;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRF 10
 |||||:||||
 Db 26 AHKSEIAHRF 35

RESULT 9

Q9PRW0 Q9PRW0 PRELIMINARY; PRT; 30 AA.
 ID Q9PRW0

AC Q9PRW0;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
 DE Alpha 1-proteinase inhibitor (Fragment).
 OS Struthio camelus (Ostrich).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
 OC Struthio.
 OX NCBI_TaxID=8801;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94341467; PubMed=8063009;
 RA Kuhn C.R., Naude R.J., Travis J., Oelofsen W.;
 RT "The isolation and partial characterization of alpha 1-proteinase
 RT inhibitor from the serum of the ostrich (Struthio camelus).";
 RL Int. J. Biochem. 26:843-853(1994).
 SQ SEQUENCE 30 AA; 3557 MW; 7775AA786BE30AC2 CRC64;

Query Match 77.6%; Score 45; DB 13; Length 30;
 Best Local Similarity 77.8%; Pred. No. 0.062;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HKSEVAHRF 10
 |||||:||||
 Db 4 HKSEIAHRF 12

RESULT 10

Q9TR98 Q9TR98 PRELIMINARY; PRT; 17 AA.
 AC Q9TR98;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
 DE Albumin (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95007849; PubMed=7923441;
 RA Miller M.J., Parmelee D.C., Benjamin T., Sechi S., Dooley K.L.,
 RA Kadlubar F.F.;
 RT "Plasma proteins as early biomarkers of exposure to carcinogenic
 RT aromatic amines";
 RL Chem.-Biol. Interact. 93:221-234(1994).
 SQ SEQUENCE 17 AA; 2024 MW; ID39F70F7D23B269 CRC64;

Query Match 74.1%; Score 43; DB 6; Length 17;
 Best Local Similarity 70.0%; Pred. No. 0.083;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRF 10
 |||||:||||
 Db 2 AYKSEIAHRF 11

RESULT 11

Q9TQ26 Q9TQ26 PRELIMINARY; PRT; 20 AA.
 AC Q9TQ26;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (T-EMBLrel. 14, Last annotation update)
 DE Albumin (Fragment).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]

```
RP SEQUENCE.
RX MEDLINE=96273610; PubMed=8690030;
RA Nicolas M.G., Fujiki K., Murayama K., Suzuki M.T., Mineki R.,
RA Hayakawa M., Yoshikawa Y., Cho F., Kanai A.;
RT "Studies on the mechanism of early onset macular degeneration in
RT cynomolgus (Macaca fascicularis) monkeys. I. Abnormal concentrations of
RT two proteins in the retina.";
RL Exp. Eye Res. 62:211-219(1996).
SQ SEQUENCE 20 AA; 2411 MW; 5F1A6ABE5918F777 CRC64;

Query Match 74.1%; Score 43; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHR 9
Db |||||
13 HKSEVAHR 20

RESULT 12
Q9POK4 PRELIMINARY; PRT; 201 AA.
ID Q9POK4
AC Q9POK4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein U0287.
GN U0287.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Seiovar 3;
RX MEDLINE=20500019; PubMed=11048724;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
RT urealyticum.";
RL Nature 407:757-762(2000).
DR EMBL; AF02125; AAF30696.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 201 AA; 23872 MW; FD0012911c4BD7E8 CRC64;

Query Match 68.1%; Score 39.5; DB 16; Length 201;
Best Local Similarity 52.6%; Pred. No. 6.6;
Matches 10; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 2 HKS-----EVAHRFK 11
Db |||
79 HKSSSLYLTNDDEVAHRFK 97

RESULT 13
Q8EQM2 PRELIMINARY; PRT; 152 AA.
ID Q8EQM2
AC Q8EQM2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical conserved protein.
GN O81673.
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
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RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; AP004598; BAC13629.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 152 AA; 18357 MW; 5FCAF143BF2D0265 CRC64;

Query Match 65.5%; Score 38; DB 16; Length 152;
Best Local Similarity 66.7%; Pred. No. 9.7;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
Db |||:: |||
19 HKSDLLHRF 27

RESULT 14
Q8I5D0 PRELIMINARY; PRT; 3209 AA.
ID Q8I5D0
AC Q8I5D0; 2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN PFL1395C.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA MCPadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser J.C., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014848; AAN36365.1; -.
KW Hypothetical protein.
SQ SEQUENCE 3209 AA; 378904 MW; DA2BBE1737C10873 CRC64;

Query Match 65.5%; Score 38; DB 5; Length 3209;
Best Local Similarity 45.5%; Pred. No. 2.9e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db :|| |||::|
791 SHKDEVSHKYE 801

RESULT 15
Q8YNI1 PRELIMINARY; PRT; 93 AA.
ID Q8YNI1
AC Q8YNI1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Asr4584.
GN ASR4584.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Muraki A.,
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RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium *Anabaena* sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003596; BAB76283.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 93 AA; 10516 MW; EA46156FB8729D0E CRC64;

Query Match 63.8%; Score 37; DB 16; Length 93;
Best Local Similarity 66.7%; Pred. No. 8.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 HKSEVAHRF 10
| :| | | |
Db 46 HAADVHRF 54

Search completed: August 29, 2003, 14:28:44
Job time : 98 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 14:24:05 ; Search time 39 Seconds
(without alignments)
27.125 Million cell updates/sec

Title: US-09-845-726a-1_copy_2_12

Perfect score: 58

Sequence: 1 AHKSEVAHFK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	58	100.0	609	1 ABHUS	serum albumin prec
2	57	98.3	608	1 ABRTS	serum albumin prec
3	54	93.1	600	2 A47391	serum albumin prec
4	54	93.1	609	2 JC5838	albumin - Mongolia
5	53	91.4	607	1 ABBS	serum albumin prec
6	48	82.8	607	1 ABSHS	serum albumin prec
7	48	82.8	607	1 ABHOS	serum albumin prec
8	48	82.8	608	2 S57632	serum albumin prec
9	47	81.0	605	1 ABPGS	serum albumin prec
10	45	77.6	615	1 ABCHS	serum albumin prec
11	43	74.1	24	2 S29749	serum albumin prec
12	40	69.0	30	2 B61511	serum albumin - do
13	39.5	68.1	201	2 E82910	serum albumin, ml
14	37	63.8	93	2 AH2378	hypothetical prote
15	36	62.1	117	2 T30740	hypothetical prote
16	36	62.1	489	2 AP3594	hypothetical prote
17	36	62.1	719	2 S63392	sensory transducti
18	36	62.1	1827	2 T16270	probable membrane
19	35	60.3	155	2 G69489	hypothetical prote
20	35	60.3	320	2 D96750	LSU ribosomal prot
21	35	60.3	672	2 H82143	unknown protein F2
22	35	60.3	969	2 T3256	methyl-accepting c
23	34	58.6	138	2 C84068	hypothetical prote
24	34	58.6	156	2 T49921	polyribonucleotide
25	34	58.6	200	2 C81282	ribosomal protein-1
26	34	58.6	222	2 A97575	hypothetical prote
27	34	58.6	222	2 A12795	hypothetical prote
28	34	58.6	385	2 C82478	conserved hypothet
29	34	58.6	391	2 T42407	probable integrase
					gephyrin homolog -

30	34	58.6	461	2 AG3151	glucose 6-phosphat
31	34	58.6	461	2 D98136	probable glucose-6
32	34	58.6	478	1 T44751	IMP dehydrogenase
33	34	58.6	488	2 G65216	hypothetical 53.4
34	34	58.6	488	2 F91261	probable enzyme YJ
35	34	58.6	488	2 B86102	probable enzyme YJ
36	34	58.6	512	2 S73457	methionine-tRNA 11
37	34	58.6	520	1 O4BOM	cholesterol monoox
38	34	58.6	1597	2 S55144	RLR1 protein - yea
39	33	56.9	91	2 T45185	hypothetical prote
40	33	56.9	182	2 T32619	hypothetical prote
41	33	56.9	185	2 E64126	hypothetical prote
42	33	56.9	219	2 C65074	probable oxidoredu
43	33	56.9	219	2 G91100	probable oxidoredu
44	33	56.9	219	2 G85945	probable oxidoredu
45	33	56.9	219	2 AG0872	probable membrane

ALIGNMENTS

RESULT 1

ABHUS

serum albumin precursor [validated] - human

N:Alternate names: preproalbumin

M:Contains: kinetensin

C:Species: Homo sapiens (man)

C>Date: 29-Jul-1981 #sequence revision 31-Jan-1997 #text change 17-Mar-2000

C:Accession: A93743; A93936; I39427; I59286; I59313; G01747; S55314; A91420; S06422;

R:Lawr, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; See

Nucleic Acids Res. 9, 6103-6114, 1981

A:Title: The sequence of human serum albumin cDNA and its expression in Escherichia c

A:Reference number: A93743; MUID:82081882; PMID:6171778

A:Accession: A93743

A:Molecule type: mRNA

A:Residues: 1-419, K', 421-609 <LAW>

A:Cross-references: EMBL:V00495; GB:J00078; GB:L00132; GB:L00133; NID:g28591; PIDN:CA

R:Dugaiczky, A.; Law, S.W.; Dennison, O.E.

Proc. Natl. Acad. Sci. U.S.A. 79, 71-75, 1982

A:Title: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA.

A:Reference number: A93936; MUID:82105994; PMID:6275391

A:Accession: A93936

A:Molecule type: mRNA

A:Residues: 1-120, 'G', 122-609 <DUG>

A:Cross-references: EMBL:V00494; NID:g28589; PIDN:CAA23753.1; PID:g28590

R:Urano, Y.; Watanabe, K.; Sakai, M.; Tamaoki, T.

J. Biol. Chem. 261, 3244-3251, 1986

A:Title: The human albumin gene. Characterization of the 5' and 3' flanking regions a

A:Reference number: I39427; MUID:86140099; PMID:2419329

A:Accession: I39427

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-26 <URA>

A:Cross-references: GB:M13075; NID:g178330; PIDN:AA51688.1; PID:g553173

R:Watkins, S.; Madson, J.; Galliano, M.; Minchiotti, L.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 91, 2275-2279, 1994

A:Title: A nucleotide insertion and frameshift cause analbuminemia in an Italian fami

A:Reference number: I59286; MUID:94181575; PMID:8134387

A:Accession: I59286

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 282-290, 'KSRFDLQ', <NAT>

A:Cross-references: GB:S69199; NID:g546032; PIDN:AAB30282.1; PID:g546033

A>Note: this frame-shift variant, designated albumin Rona, leads to analbuminemia

R:Madison, J.; Galliano, M.; Watkins, S.; Minchiotti, L.; Porta, F.; Rossi, A.; Putna

Proc. Natl. Acad. Sci. U.S.A. 91, 6476-6480, 1994

A:Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox

A:Reference number: I59313; MUID:94294404; PMID:8022807

A:Accession: I59313

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 589-590, 'ALPRVKNLLIQVKLP', <MAD>

A:Cross-references: GB:S70799; NID:g547231; PIDN:AAB31177.1; PID:g547232

A;Note: this frame-shift variant is designated albumin Bazzano; four additional variants submitted to the EMBL Data Library, March 1995
R;Menaya, J.; Parrilla, R.; Ayuso, M.S.
A;Reference number: G08292
A;Accession: G01747
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-120, 'G', 122-455 <MEN>
A;Cross-references: EMBL:U22961; NID:g763428; PID:g763431
R;Ledgerwood, E.C.; George, P.M.; Peach, R.J.; Brennan, S.O.
Biochem. J. 308, 321-325, 1995
A;Title: Endoproteolytic processing of recombinant proalbumin variants by the yeast *Kex2*
A;Reference number: S55314; MUID:95275251; PMID:7755581
A;Accession: S55314
A;Molecule type: protein
A;Residues: 19-27 <LED>
R;Meloun, B.; Moravek, L.; Kostka, V.
FEBS Lett. 58, 134-137, 1975
A;Title: Complete amino acid sequence of human serum albumin.
A;Reference number: A91420; MUID:76187907; PMID:1225573
A;Accession: A91420
A;Molecule type: protein
A;Residues: 25-117, 'Eq', 120-154, 'Q', 156-193, 'E', 195-387, 'H', 389-390, 'Y', 392-393, 'A', 395-396, 'S', 398-400, 'L', 402-403, 'I', 405-406, 'V', 408-409, 'M', 411-412, 'K', 414-415, 'R', 417-418, 'G', 420-421, 'D', 423-424, 'N', 426-427, 'C', 429-430, 'P', 432-433, 'T', 435-436, 'S', 438-439, 'A', 441-442, 'G', 444-445, 'K', 447-448, 'R', 450-451, 'Q', 453-454, 'E', 456-457, 'D', 459-460, 'N', 462-463, 'K', 465-466, 'R', 468-469, 'G', 471-472, 'D', 474-475, 'E', 477-478, 'K', 480-481, 'R', 483-484, 'G', 486-487, 'D', 489-490, 'N', 492-493, 'K', 495-496, 'R', 498-499, 'G', 501-502, 'D', 504-505, 'K', 507-508, 'R', 510-511, 'Q', 513-514, 'E', 516-517, 'D', 519-520, 'K', 522-523, 'R', 525-526, 'G', 528-529, 'D', 531-532, 'K', 534-535, 'R', 537-538, 'G', 540-541, 'D', 543-544, 'K', 546-547, 'R', 549-550, 'G', 552-553, 'D', 555-556, 'K', 558-559, 'R', 561-562, 'G', 564-565, 'D', 567-568, 'K', 570-571, 'E', 573-574, 'D', 576-577, 'K', 579-580, 'R', 582-583, 'G', 585-586, 'D', 588-589, 'K', 591-592, 'R', 594-595, 'G', 597-598, 'D', 600-601, 'K', 603-604, 'R', 606-607, 'G', 609-610, 'D', 612-613, 'K', 615-616, 'R', 618-619, 'G', 621-622, 'D', 624-625, 'K', 627-628, 'R', 630-631, 'G', 633-634, 'D', 636-637, 'K', 639-640, 'R', 642-643, 'G', 645-646, 'D', 648-649, 'K', 651-652, 'R', 654-655, 'G', 657-658, 'D', 660-661, 'K', 663-664, 'R', 666-667, 'G', 669-670, 'D', 672-673, 'K', 675-676, 'R', 678-679, 'G', 681-682, 'D', 684-685, 'K', 687-688, 'R', 690-691, 'G', 693-694, 'D', 696-697, 'K', 699-700, 'R', 702-703, 'G', 705-706, 'D', 708-709, 'K', 711-712, 'R', 714-715, 'G', 717-718, 'D', 720-721, 'K', 723-724, 'R', 726-727, 'G', 729-730, 'D', 732-733, 'K', 735-736, 'R', 738-739, 'G', 741-742, 'D', 744-745, 'K', 747-748, 'R', 750-751, 'G', 753-754, 'D', 756-757, 'K', 759-760, 'R', 762-763, 'G', 765-766, 'D', 768-769, 'K', 771-772, 'R', 774-775, 'G', 777-778, 'D', 780-781, 'K', 783-784, 'R', 786-787, 'G', 789-790, 'D', 792-793, 'K', 795-796, 'R', 798-799, 'G', 801-802, 'D', 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F;166-174/Product: kinetensin #status experimental <KIP>
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F;413-592/Domain: serum albumin repeat homology <SA3>
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Query Match 100.0%; Score 58; DB 1; Length 609;
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RESULT 2
ABRTS
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C;Accession: A93872; A92211; A91946; A91940; C45800; I57621; A03233
R;Sargent, T.D.; Yang, M.; Bonner, J.
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A;Title: Nucleotide sequence of cloned rat serum albumin messenger RNA.
A;Reference number: A93872; MUID:81223722; PMID:7017772
A;Accession: A93872
A;Molecule type: mRNA
A;Residues: 1-608 <SAR>
A;Cross-references: GB:J00698; NID:955627; PIDN:CAA24532.1; PID:g55628
R;Strauss, A.W.; Bennett, C.D.; Donohue, A.M.; Rodkey, J.A.; Alberts, A.W.
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A;Reference number: A92211; MUID:77249657; PMID:893447
A;Note: cleavages during protein maturation
A;Accession: A92211
A;Molecule type: protein
A;Residues: 1-38 <STR>
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A;Reference number: A91946; MUID:78109429; PMID:564345
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A;Residues: 25-222 <ISI>
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A;Reference number: A91940; MUID:76260153; PMID:956149
A;Accession: A91940
A;Molecule type: protein
A;Residues: 223-288;572-608 <IS2>
A;Note: 262-Leu was also found
R;Aoyagi, Y.; Ikenaka, T.; Ichida, F.
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A;Title: Copper(II)-binding ability of human alpha-fetoprotein.
A;Reference number: A90758; MUID:79001617; PMID:80265
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A;Title: Structures of histamine-releasing peptides formed by the action of acid proteas
A;Reference number: A45800; MUID:89341406; PMID:2474609
A;Accession: C45800
A;Status: preliminary
A;Molecule type: protein
A;Residues: 166-173 <CAR>
R;Heard, J.
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A;Title: Determinants of rat albumin promoter tissue specificity analyzed by an improved
A;Reference number: I57621; MUID:87286876; PMID:3475566
A;Accession: I57621
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-5 <RES>
A;Cross-references: GB:M16825; NID:g202828; PIDN:AAA40712.1; PID:g554412
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-608/Product: serum albumin #status experimental <MAT>
F;29-202/Domain: serum albumin repeat homology <SA1>
F;221-394/Domain: serum albumin repeat homology <SA2>
F;413-592/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status experimental
F;77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-393,4

Query Match 98.3%; Score 57; DB 1; Length 608;
Best Local Similarity 90.9%; Pred. No. 0.006;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
|||||
Db 26 AHKSEVAHRFK 36

RESULT 3
A47391
serum albumin precursor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C;Accession: A47391
R;Watkins, S.; Sakamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwulet, J.; Putnam,
Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993
A;Title: cDNA and protein sequence of polymorphic macaque albumins that differ in b11
A;Reference number: A47391; MUID:93211971; PMID:8460152
A;Contents: B/B homozygote
A;Accession: A47391
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-609 <MAT>
A;Cross-references: GB:M90463; NID:g342294; PIDN:AAA36906.1; PID:g342295
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIN:128280, NCBI:128281)
C;Superfamily: serum albumin; serum albumin repeat homology
F;21-194/Domain: serum albumin repeat homology <SA1>
F;213-386/Domain: serum albumin repeat homology <SA2>
F;405-584/Domain: serum albumin repeat homology <SA3>

Query Match 93.1%; Score 54; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRFK 11
|||||
Db 19 HKSEVAHRFK 28

RESULT 4
JC5838
albumin - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 03-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 19-May-2000
C;Accession: JC5838
R;Yoshida, K.; Seto-Ohshima, A.; Sinohara, H.
DNA Res. 4, 351-354, 1997
A;Title: Sequencing of cDNA encoding serum albumin and its extrahepatic synthesis in
A;Reference number: JC5838; MUID:98116663; PMID:9455485
A;Accession: JC5838
A;Molecule type: mRNA
A;Residues: 1-609 <YOS>
A;Cross-references: DDBJ:AB006197; NID:g2317277; PIDN:BAA21765.1; PID:g2317278
A;Experimental source: liver
C;Superfamily: serum albumin; serum albumin repeat homology
F;222-395/Domain: serum albumin repeat homology <SA2>

Query Match 93.1%; Score 54; DB 2; Length 609;
Best Local Similarity 81.8%; Pred. No. 0.023;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
|||||:||||:
DB 27 AHKSEIAHRYK 37

RESULT 5
ABBS
serum albumin precursor [validated] - bovine
N:Alternate names: 67K protein; preproalbumin
C:Species: Bos primigenius taurus (Cattle)
C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000
C:Accession: A38885; A36401; A91258; B60808; S10780; D45800; A26693; A90309; A91458; A94
R:Holowachuk, E.W.; Stoltzenberg, J.K.; Reed, R.G.; Peters Jr., T.
submitted to the EMBL Data Library, August 1991
A:Description: Bovine serum albumin: cDNA sequence and expression.
A:Reference number: A38885
A:Accession: A38885
A:Molecule type: mRNA
A:Residues: 1-607 <HOL>
A:Cross-references: EMBL:M73215
R:Hirayama, K.; Akashi, S.; Furuya, M.; Fukuhara, K.
Biochem. Biophys. Res. Commun. 173, 639-646, 1990
A:Title: Rapid confirmation and revision of the primary structure of bovine serum albumin
A:Reference number: A36401; MUID:91083649; PMID:2260975
A:Accession: A36401
A:Molecule type: protein
A:Residues: 25-41, 'H', '43-189, 'E', 191-213, 'T', 215-323, 'D', 325-393, 'TS', 396-607 <HIR>
R:Macgillivray, R.T.A.; Chung, D.W.; Davie, E.W.
Eur. J. Biochem. 98, 477-485, 1979
A:Title: Biosynthesis of bovine plasma proteins in a cell-free system.
A:Reference number: A91258; MUID:80024278; PMID:488109
A:Accession: A91258
A:Molecule type: protein
A:Residues: 1-32 <MAG>
R:Hsieh, J.C.; Lin, F.P.; Tam, M.F.
Anal. Biochem. 170, 1-8, 1988
A:Title: Electrophoretic filter from an analytical isoelectrofocusing gel
A:Reference number: A60808; MUID:88267456; PMID:3389500
A:Accession: B60808
A:Molecule type: protein
A:Residues: 25-41 <HSI>
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albumin
A:Reference number: S10780; MUID:90336641; PMID:2379503
A:Accession: S10780
A:Molecule type: protein
A:Residues: 25-41, 'H', '43-57, 59-64 <STR>
R:Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A:Title: Structures of histamine-releasing peptides formed by the action of acid proteases
A:Reference number: A45800; MUID:89341406; PMID:2474609
A:Accession: D45800
A:Molecule type: protein
A:Residues: 163-172 <CAR>
R:Carraway, R.E.; Mitra, S.P.; Cochrane, D.E.
J. Biol. Chem. 262, 5968-5973, 1987
A:Title: Structure of a biologically active neurotensin-related peptide obtained from pe
A:Reference number: A26693; MUID:87194805; PMID:2437111
A:Accession: A26693
A:Molecule type: protein
A:Residues: 165-172, 'L', <CA2>
R:Reed, R.G.; Putnam, F.W.; Peters Jr., T.
Biochem. J. 191, 867-868, 1980
A:Title: Sequence of residues 400-403 of bovine serum albumin.
A:Reference number: A90309; MUID:82023364; PMID:7283978
A:Accession: A90309
A:Molecule type: protein
A:Residues: 402-433 <REE>

R:Brown, J.R.
Fed. Proc. 34, 591, 1975
A:Title: Structure of bovine serum albumin.
A:Reference number: A91458
A:Accession: A91458
A:Molecule type: protein
A:Residues: 25-41, 'H', '43-117, 'EQ', 120-179, 181-189, 'E', 191-194, 'A', 196-213, 'T', 215-288
R:Brown, J.R.
submitted to the Atlas, April 1975
A:Reference number: A94551
A:Accession: A94551
A:Molecule type: protein
A:Residues: 190-195 <BR2>
R:Brown, J.R.
Fed. Proc. 33, 1389, 1974
A:Reference number: A91457
A:Contents: annotation; disulfide bonds
R:Werlen, R.C.; Offord, R.E.; Rose, K.
Biochem. J. 302, 907-911, 1994
A:Title: Preparation and characterization of novel substrates of insulin proteinase (C
A:Reference number: S55232; MUID:95031935; PMID:7945219
A:Accession: S55232
A:Status: preliminary
A:Molecule type: protein
A:Residues: 529-536; 569-572 <WER>
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; copper binding; duplication; plasma
F:1-18/Domain: signal sequence #status experimental <SIG>
F:19-24/Domain: propeptide #status experimental <PRO>
F:25-607/Product: serum albumin #status experimental <MPT>
F:229-203/Domain: serum albumin repeat homology <SA1>
F:220-393/Domain: serum albumin repeat homology <SA2>
F:412-591/Domain: serum albumin repeat homology <SA3>
F:27/Binding site: copper (His) #status predicted
F:77-86, 99-115, 114-125, 147-192, 191-200, 223-269, 268-276, 288-302, 301-312, 339-384, 383-393

Query Match 91.4%; Score 53; DB 1; Length 607;
Best Local Similarity 90.0%; Pred. No. 0.035;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRFK 11
|||||:||||:
DB 27 HKSEIAHRYK 36

RESULT 6
ABBS
serum albumin precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C:Accession: S06936
R:Brown, W.M.; Dziedzielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 10495, 1989
A:Title: Nucleotide and deduced amino acid sequence of sheep serum albumin.
A:Reference number: S06936; MUID:90098888; PMID:2602160
A:Accession: S06936
A:Molecule type: mRNA
A:Residues: 1-607 <BRO>
A:Cross-references: EMBL:X17055; NID:gl386; PIDN:CA34903.1; PID:91387
C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper
teroid hormones (weak bonds with these hormones promote their transfer across the mem
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; metal binding; plasma
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status predicted <PRO>
F:25-607/Product: serum albumin repeat homology <SA1>
F:229-203/Domain: serum albumin repeat homology <SA2>
F:220-393/Domain: serum albumin repeat homology <SA3>
F:412-591/Domain: serum albumin repeat homology <SA3>
F:27/Binding site: copper (His) #status predicted
F:77-86, 99-115, 114-125, 147-192, 191-200, 223-269, 268-276, 288-302, 301-312, 339-384, 383-393

Query Match 82.8%; Score 48; DB 1; Length 607;
 Best Local Similarity 88.9%; Pred. No. 0.32;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
 |||||
 DB 27 HKSEIAHRF 35

RESULT 7

ABHOS

serum albumin precursor - horse
 C:Species: Equus caballus (domestic horse)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
 C:Accession: S34053
 R:Ho, J.X.; Holowachuk, E.W.; Norton, E.J.; Twigg, P.D.; Carter, D.C.
 Eur. J. Biochem. 215, 205-212, 1993
 A:Title: X-ray and primary structure of horse serum albumin (Equus caballus) at 0.27-nm
 A:Reference number: S34053; MUID:93345495; PMID:8344282
 A:Accession: S34053
 A:Molecule type: mRNA
 A:Residues: 1-607 <HOA>
 A:Cross-references: GB:X74045; NID:G399671; PIDN:CAA52194.1; PID:G399672
 C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, teroid hormones (weak bonds with these hormones promote their transfer across the membrane)
 C:Superfamily: serum albumin; serum albumin repeat homology
 C:Keywords: carrier protein; duplication; metal binding; plasma
 F:19-24/Domain: signal sequence #status predicted <PRO>
 F:19-24/Domain: propeptide #status predicted <SIG>
 F:25-607/Product: serum albumin #status predicted <MAT>
 F:29-301/Domain: serum albumin repeat homology <SA1>
 F:220-393/Domain: serum albumin repeat homology <SA2>
 F:412-591/Domain: serum albumin repeat homology <SA3>
 F:27/Binding site: copper (His) #status predicted
 F:77-86,99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392,4
 F:263/Binding site: bilirubin (Lys) #status predicted

Query Match 82.8%; Score 48; DB 1; Length 607;
 Best Local Similarity 88.9%; Pred. No. 0.32;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
 |||||
 DB 27 HKSEIAHRF 35

RESULT 8

S57632

serum albumin precursor - cat
 C:Species: Felis silvestris catus (domestic cat)
 C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999
 C:Accession: JC4660; S57632
 R:Hilger, C.; Grigioni, F.; Hentges, F.
 Gene 169, 295-296, 1996
 A:Title: Sequence of the gene encoding cat (Felis domesticus) serum albumin.
 A:Reference number: JC4660; MUID:96194824; PMID:8647469
 A:Accession: JC4660
 A:Molecule type: mRNA
 A:Residues: 1-608 <HI2>
 A:Cross-references: EMBL:X84842; NID:9886484; PIDN:CAA59279.1; PID:9886485
 A:Experimental source: liver
 C:Comment: This protein is the major protein component in plasma. It functions as a multiein has 35 conserved cysteine residues.
 C:Superfamily: serum albumin; serum albumin repeat homology
 C:Keywords: liver; plasma
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRO>
 F:25-608/Product: serum albumin #status predicted <MAT>
 F:29-202/Domain: serum albumin repeat homology <SA1>
 F:221-394/Domain: serum albumin repeat homology <SA2>
 F:413-592/Domain: serum albumin repeat homology <SA3>

Query Match 82.8%; Score 48; DB 2; Length 608;

Best Local Similarity 80.0%; Pred. No. 0.32;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRF 10
 |||||
 DB 26 AHQSEIAHRF 35

RESULT 9

ABPGS

serum albumin precursor - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
 C:Accession: S01382; A61006
 R:Weinstock, J.; Baldwin, G.S.
 Nucleic Acids Res. 16, 9045, 1988
 A:Title: Nucleotide sequence of porcine liver albumin.
 A:Reference number: S01382; MUID:89016582; PMID:3174440
 A:Accession: S01382
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-605 <WEI>
 A:Cross-references: EMBL:X12422; NID:91875; PIDN:CAA30970.1; PID:9833798
 R:Limeback, H.; Sakarya, H.; Chu, W.; Mackinnon, M.
 J. Bone Miner. Res. 4, 235-241, 1989
 A:Title: Serum albumin and its acid hydrolysis peptides dominate preparations of mine
 A:Reference number: A61006; MUID:89269769; PMID:2728927
 A:Accession: A61006
 A:Molecule type: protein
 A:Residues: 23-51, 'X', 53-54; 'XXXGY', 146, 'E', 148, 'E', 150-151, 'XVN', 155 <LIM>
 A:Experimental source: dental enamel
 A:Note: albumin and other serum proteins are also found in bone
 C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper teroid hormones (weak bonds with these hormones promote their transfer across the membrane)
 C:Superfamily: serum albumin; serum albumin repeat homology
 C:Keywords: carrier protein; duplication; metal binding; plasma
 F:1-16/Domain: signal sequence (fragment) #status predicted <SIG>
 F:17-22/Domain: propeptide #status predicted <PRO>
 F:23-605/Product: serum albumin #status predicted <MAT>
 F:27-199/Domain: serum albumin repeat homology <SA1>
 F:218-391/Domain: serum albumin repeat homology <SA2>
 F:410-589/Domain: serum albumin repeat homology <SA3>
 F:75-84,97-113,112-123,145-190,189-198,221-267,266-274,286-300,299-310,337-382,381-39
 F:761/Binding site: bilirubin (Lys) #status predicted

Query Match 81.0%; Score 47; DB 1; Length 605;
 Best Local Similarity 80.0%; Pred. No. 0.49;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 11
 |||||
 DB 25 YKSEIAHRF 34

RESULT 10

ABCHS

serum albumin precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
 C:Accession: S15571; A05078; A13451
 R:Cassady, A.I.; Salkild, C.K.; Baverstock, P.; Wallace, J.C.
 submitted to the EMBL Data Library, July 1991
 A:Reference number: S15571
 A:Accession: S15571
 A:Molecule type: mRNA
 A:Residues: 1-615 <CAS>
 A:Cross-references: EMBL:X60688; NID:963747; PIDN:CAA43098.1; PID:963748
 R:Hache, R.J.G.; Wiskocil, R.; Vasa, M.; Roy, R.N.; Lau, P.C.K.; Deeley, R.G.
 J. Biol. Chem. 258, 4556-4564, 1983
 A:Title: The 5' noncoding and flanking regions of the avian very low density apolipop
 A:Reference number: A05078; MUID:83161037; PMID:6187737
 A:Accession: A05078
 A:Molecule type: DNA

A;Residues: 1-28 <HAC>
 A;Cross-references: GB:V00381; NID:g63038; PIDN:CAA23680.1; PID:g63039
 R;Rosen, A.M.; Geller, D.M.
 Biochem. Biophys. Res. Commun. 78, 1060-1066, 1977
 A;Title: Chicken microsomal albumin: amino terminal sequence of chicken proalbumin.
 A;Reference number: A13451; MUID:78019943; PMID:911327
 A;Accession: A13451

A;Molecule type: protein
 A;Residues: 19-23 'M', 25-30 <ROS>
 C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, monees (weak bonds with these hormones promote their transfer across the membranes), thyra
 C;Superfamily: serum albumin; serum albumin repeat homology
 C;Keywords: carrier protein; duplication; metal binding; plasma
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-26/Domain: propeptide #status predicted <PRO>
 F:27-613/Product: serum albumin #status predicted <MAT>
 F:32-206/Domain: serum albumin repeat homology <SA1>
 F:225-398/Domain: serum albumin repeat homology <SA2>
 F:417-596/Domain: serum albumin repeat homology <SA3>
 F:30/Binding site: copper (HIs) #status predicted
 F:80-89,102-118,117-128,152-197,196-205,228-274,273-281,293-307,306-317,344-389,388-397,

Query Match 77.6%; Score 45; DB 1; Length 615;
 Best Local Similarity 77.8%; Pred. No. 1.2;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
 |||||:||||
 DB 30 HKSEIAHRY 38

RESULT 11

S29749
 serum albumin - dog
 C;Species: Canis lupus familiaris (dog)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
 C;Accession: S29749
 R;Dixon, J.W.; Sarkar, B.
 J. Biol. Chem. 249, 5872-5877, 1974
 A;Title: Isolation, amino acid sequence and copper(II)-binding properties of peptide (1-
 A;Reference number: S29749; MUID:75011422; PMID:4414013
 A;Accession: S29749
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-24 <DIX>
 C;Superfamily: serum albumin; serum albumin repeat homology

Query Match 74.1%; Score 43; DB 2; Length 24;
 Best Local Similarity 70.0%; Pred. No. 0.094;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRF 10
 |::|||:||||
 DB 2 AYKSEIAHRY 11

RESULT 12

B61511
 serum albumin, milk-derived - Australian echidna (fragment)
 C;Species: Tachyglossus aculeatus (Australian echidna)
 C;Date: 09-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000
 C;Accession: B61511
 R;Teahan, C.G.; McKenzie, H.A.; Griffiths, M.
 Comp. Biochem. Physiol. B 99, 99-118, 1991
 A;Title: Some monotreme milk "whey" and blood proteins.
 A;Reference number: A61511; MUID:92070088; PMID:1959333
 A;Accession: B61511
 A;Status: preliminary

A;Molecule type: protein
 A;Residues: 1-30 <GRI>
 C;Superfamily: serum albumin; serum albumin repeat homology
 C;Keywords: milk

Query Match 69.0%; Score 40; DB 2; Length 30;
 Best Local Similarity 63.6%; Pred. No. 0.44;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRF 11
 |::|||:||||
 DB 2 AQKSELGHRYK 12

RESULT 13

E82910
 hypothetical protein UU287 [imported] - Ureaplasma urealyticum
 C;Species: Ureaplasma urealyticum
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C;Accession: E82910
 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to GenBank, February 2000
 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a
 A;Reference number: A82870
 A;Accession: E82910
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-201 <GLA>
 A;Cross-references: GB:AE002125; GB:AF222894; NID:g6899253; PIDN:AAF30696.1; GSPDB:GN
 A;Experimental source: serovar 3; biovar 1
 C;Genetics:
 A;Gene: UU287
 A;Genetic code: SGC3

Query Match 68.1%; Score 39.5; DB 2; Length 201;
 Best Local Similarity 52.6%; Pred. No. 4.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 2 HKS-----EVAHRFK 11
 |||||
 DB 79 HKSSSLYLTNDDEVAHRFK 97

RESULT 14

AH2378
 hypothetical protein asr4584 [imported] - Nostoc sp. (strain PCC 7120)
 C;Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C;Accession: AH2378
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
 DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AH2378
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-93 <KUR>
 A;Cross-references: GB:BA000019; PIDN:BA076283.1; PID:g17133720; GSPDB:GN00179
 A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: asr4584

Query Match 63.8%; Score 37; DB 2; Length 93;
 Best Local Similarity 66.7%; Pred. No. 5.5;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
 |::|||:||||
 DB 46 HAADVHRF 54

RESULT 15

T30740
 hypothetical protein 138R - Molluscum contagiosum virus 1
 N;Alternate names: MC138R
 C;Species: Molluscum contagiosum virus 1

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T30740
R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A>Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A:Reference number: Z20876; MUID:96325459; PMID:8670425
A:Accession: T30740
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-117 <SEN>
A:Cross-references: EMBL:U60315; PIDN:AAC55266.1
C:Genetics:
A:Note: MC138R
C:Superfamily: variola major virus 6R protein

Query Match 62.1%; Score 36; DB 2; Length 117;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AHKSEVAHR 9
| | | | |
DB 24 AHKSAFAHR 32

Search completed: August 29, 2003, 14:29:28
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: August 29, 2003, 14:27:05 ; Search time 24 Seconds
(without alignments)
13.562 Million cell updates/sec

Title: US-09-845-726A-1_COPY_2_12

Perfect score: 58

Sequence: 1 AHKSEVAHRFK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141812 seqs, 29589763 residues

Total number of hits satisfying chosen parameters: 141812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents_AA.New.*
1: /cgn2.6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2.6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2.6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2.6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2.6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2.6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2.6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	54	6 US-10-273-573-10524	Sequence 10524, A
2	58	100.0	76	6 US-10-273-573-5999	Sequence 5999, Ap
3	58	100.0	133	6 US-10-273-573-5979	Sequence 5979, Ap
4	58	100.0	134	6 US-10-273-573-5922	Sequence 5922, Ap
5	58	100.0	156	6 US-10-273-573-5921	Sequence 5921, Ap
6	58	100.0	192	6 US-10-273-573-5924	Sequence 5924, Ap
7	58	100.0	214	6 US-10-273-573-5923	Sequence 5923, Ap
8	58	100.0	289	6 US-10-273-573-5569	Sequence 5569, Ap
9	58	100.0	401	6 US-10-273-573-5935	Sequence 5935, Ap
10	58	100.0	520	6 US-10-273-573-5926	Sequence 5926, Ap
11	58	100.0	550	6 US-10-273-573-5927	Sequence 5927, Ap
12	58	100.0	585	1 PCT-US03-18896-26	Sequence 26, Appl
13	58	100.0	585	1 PCT-US03-19902-3	Sequence 3, Appl
14	58	100.0	585	6 US-10-462-262-26	Sequence 26, Appl
15	58	100.0	585	6 US-10-602-141-3	Sequence 3, Appl
16	58	100.0	585	6 US-10-424-999-11	Sequence 11, Appl
17	58	100.0	585	6 US-10-425-000-31	Sequence 31, Appl
18	58	100.0	604	6 US-10-408-765A-55	Sequence 55, Appl
19	58	100.0	609	6 US-10-408-765A-2	Sequence 2, Appl
20	58	100.0	609	6 US-10-609-346-12	Sequence 12, Appl
21	58	100.0	609	7 US-60-490-890-752	Sequence 752, App
22	58	100.0	609	7 US-60-490-419-1	Sequence 1, Appl
23	58	100.0	609	7 US-60-490-149-1	Sequence 1, Appl
24	58	100.0	672	6 US-10-424-999-15	Sequence 15, Appl
25	58	100.0	672	6 US-10-425-000-35	Sequence 35, Appl
26	58	100.0	674	6 US-10-424-999-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-10-273-573-10524
; Sequence 10524, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 10524
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-273-573-10524

Query Match: 100.0%; Score 58; DB 6; Length 54;

Best Local Similarity 100.0%; Pred. No. 6.6e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 AHKSEVAHRFK 11

Db 21 AHKSEVAHRFK 31

RESULT 2

US-10-273-573-5999
; Sequence 5999, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5999
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens

Sequence 34, Appl
Sequence 10514, A
Sequence 17, Appl
Sequence 37, Appl
Sequence 18, Appl
Sequence 38, Appl
Sequence 13, Appl
Sequence 10, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 5928, Ap
Sequence 5931, Ap
Sequence 2, Appl
Sequence 6000, Ap
Sequence 5930, Ap
Sequence 5929, Ap
Sequence 5708, Ap

6 US-10-425-000-34
6 US-10-273-573-10514
6 US-10-424-999-17
6 US-10-425-000-37
6 US-10-424-999-18
6 US-10-425-000-38
6 US-10-424-999-13
6 US-10-425-000-33
6 US-10-609-346-10
6 US-10-609-346-4
6 US-10-609-346-6
6 US-10-273-573-5928
6 US-10-273-573-5931
6 US-10-609-346-8
6 US-10-273-573-5930
6 US-10-273-573-5930
6 US-10-273-573-5929
6 US-10-273-573-5708

27 58 100.0
28 58 100.0
29 58 100.0
30 58 100.0
31 58 100.0
32 58 100.0
33 58 100.0
34 58 100.0
35 58 100.0
36 58 100.0
37 58 100.0
38 58 100.0
39 58 100.0
40 58 100.0
41 58 100.0
42 58 100.0
43 58 100.0
44 58 100.0
45 58 100.0

US-10-273-573-5999

Query Match 100.0%; Score 58; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
|||||

Db 37 AHKSEVAHRFK 47

RESULT 3

US-10-273-573-5979
; Sequence 5979, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5979
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (112)..(127)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by EMATRIX,
; OTHER INFORMATION: accession number PR00802a, p-value=2.324e-14, raw score of 12.17
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (30)..(132)
; OTHER INFORMATION: Serum albumin family domain identified by PFam, accession
; OTHER INFORMATION: name transport_prot, E-value=2.8e-10, PFam score of 47.6
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(133)
; OTHER INFORMATION: Xaa = x or * as defined in Table 2

US-10-273-573-5979

Query Match 100.0%; Score 58; DB 6; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
|||||

Db 28 AHKSEVAHRFK 38

RESULT 4

US-10-273-573-5922
; Sequence 5922, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5922
; LENGTH: 134
; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (58)..(134)

; OTHER INFORMATION: Serum albumin family domain identified by PFam, accession
; OTHER INFORMATION: name transport_prot, E-value=0.00037, PFam score of -21.7
US-10-273-573-5922

Query Match 100.0%; Score 58; DB 6; Length 134;

Best Local Similarity 100.0%; Pred. No. 0.0002;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11

Db 56 AHKSEVAHRFK 66

RESULT 5

US-10-273-573-5921
; Sequence 5921, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5921
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (120)..(135)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by EMATRIX,
; OTHER INFORMATION: accession number PR00802a, p-value=1.000e-19, raw score of 12.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (35)..(153)
; OTHER INFORMATION: Serum albumin family domain identified by PFam, accession
; OTHER INFORMATION: name transport_prot, E-value=3.7e-26, PFam score of 100.3
US-10-273-573-5921

Query Match 100.0%; Score 58; DB 6; Length 156;

Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11

Db 33 AHKSEVAHRFK 43

RESULT 6

US-10-273-573-5924
; Sequence 5924, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5924

```
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (130)..(154)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by eMATRIX,
; OTHER INFORMATION: accession number PR00802B, p-value=6.294e-24, raw score of 16.51
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (56)..(185)
; OTHER INFORMATION: Serum albumin family domain identified by Pfam, accession
; OTHER INFORMATION: name transport_prot, E-value=6.3e-42, Pfam score of 152.7
US-10-273-573-5924
```

```
Query Match 100.0%; Score 58; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AHKSEVAHRFK 11
Db 54 AHKSEVAHRFK 64
```

RESULT 7

```
US-10-273-573-5923
; Sequence 5923, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5923
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (149)..(173)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by eMATRIX,
; OTHER INFORMATION: accession number PR00802B, p-value=6.294e-24, raw score of 16.51
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (40)..(204)
; OTHER INFORMATION: Serum albumin family domain identified by Pfam, accession
; OTHER INFORMATION: name transport_prot, E-value=1.2e-71, Pfam score of 251.5
US-10-273-573-5923
```

```
Query Match 100.0%; Score 58; DB 6; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AHKSEVAHRFK 11
Db 38 AHKSEVAHRFK 48
```

RESULT 8

```
US-10-273-573-5569
; Sequence 5569, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
```

```
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5569
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (125)..(140)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by eMATRIX,
; OTHER INFORMATION: accession number PR00802A, p-value=3.066e-09, raw score of 12.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (41)..(230)
; OTHER INFORMATION: Serum albumin family domain identified by Pfam, accession
; OTHER INFORMATION: name transport_prot, E-value=6.6e-26, Pfam score of 99.5
; NAME/KEY: misc.feature
; LOCATION: (1)..(289)
; OTHER INFORMATION: Xaa - X or * as defined in Table 2
US-10-273-573-5569
```

```
Query Match 100.0%; Score 58; DB 6; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AHKSEVAHRFK 11
Db 38 AHKSEVAHRFK 48
```

RESULT 9

```
US-10-273-573-5925
; Sequence 5925, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5925
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (161)..(185)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by eMATRIX,
; OTHER INFORMATION: accession number PR00802B, p-value=6.294e-24, raw score of 16.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (41)..(384)
; OTHER INFORMATION: Serum albumin family domain identified by Pfam, accession
; OTHER INFORMATION: name transport_prot, E-value=2.7e-102, Pfam score of 353.3
US-10-273-573-5925
```

```
Query Match 100.0%; Score 58; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AHKSEVAHRFK 11
Db 39 AHKSEVAHRFK 49
```

```
RESULT 10
US-10-273-573-5926
; Sequence 5926, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5926
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (158)..(210)
; OTHER INFORMATION: Serum albumin family proteins domain identified by eMATRIX,
; accession number BL00212, p-value=1.000e-40, raw score of 30.19
US-10-273-573-5926
; NAME/KEY: DOMAIN
; LOCATION: (44)..(503)
; OTHER INFORMATION: Serum albumin family domain identified by Pfam, accession
; number transport_prot, E-value=2.6e-126, Pfam score of 433.1
US-10-273-573-5926

Query Match      100.0%; Score 58; DB 6; Length 520;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AHKSEVAHRFK 11
Db      42 AHKSEVAHRFK 52
|||||

RESULT 11
US-10-273-573-5927
; Sequence 5927, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5927
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (188)..(240)
; OTHER INFORMATION: Serum albumin family proteins domain identified by eMATRIX,
; accession number BL00212, p-value=1.000e-40, raw score of 30.19
US-10-273-573-5927
; NAME/KEY: DOMAIN
; LOCATION: (30)..(534)
; OTHER INFORMATION: Serum albumin family domain identified by Pfam, accession
; number transport_prot, E-value=1.2e-150, Pfam score of 513.9
US-10-273-573-5927
```

```
Query Match      100.0%; Score 58; DB 6; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AHKSEVAHRFK 11
Db      28 AHKSEVAHRFK 38
|||||

RESULT 12
PCT-US03-18896-26
; Sequence 26, Application PC/TUS0318896
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052W01
; CURRENT APPLICATION NUMBER: PCT/US03/18896
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
PCT-US03-18896-26

Query Match      100.0%; Score 58; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AHKSEVAHRFK 11
Db      2 AHKSEVAHRFK 12
|||||

RESULT 13
PCT-US03-19902-3
; Sequence 3, Application PC/TUS0319902
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation
; TITLE OF INVENTION: SERUM PROTEIN-ASSOCIATED TARGET-SPECIFIC
; LIGANDS AND IDENTIFICATION METHOD THEREFOR
; FILE REFERENCE: 10280-058W01
; CURRENT APPLICATION NUMBER: PCT/US03/19902
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US 60/390,657
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
PCT-US03-19902-3

Query Match      100.0%; Score 58; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AHKSEVAHRFK 11
Db      2 AHKSEVAHRFK 12
|||||

RESULT 14
US-10-462-262-26
; Sequence 26, Application US/10462262
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
```

```
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-262-26
```

```
Query Match 100.0%; Score 58; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
```

```
RESULT 15
US-10-602-141-3
; Sequence 3, Application US/10602141
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; TITLE OF INVENTION: SERUM PROTEIN-ASSOCIATED TARGET-SPECIFIC
; TITLE OF INVENTION: LIGANDS AND IDENTIFICATION METHOD THEREFOR
; FILE REFERENCE: 10280-058001
; CURRENT APPLICATION NUMBER: US/10/602,141
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US 60/390,657
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-602-141-3
```

```
Query Match 100.0%; Score 58; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
```

```
Search completed: August 29, 2003, 14:38:01
Job time : 25 secs
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OM protein - protein search, using sw model

Run on: August 29, 2003, 14:26:35 ; Search time 378 Seconds
(without alignments)
25,328 Million cell updates/sec

Title: US-09-845-726A-1_COPY_2_12

Perfect score: 58

Sequence: 1 AHKSEVAHREK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5580241 seqs, 870357830 residues

Total number of hits satisfying chosen parameters: 5580241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
1	58	100.0	11 1	PCT-US00-26952-4
2	58	100.0	11 1	PCT-US02-04275-4

3	58	100.0	11	PCT-US02-37136-4	Sequence 4, Appli
4	58	100.0	11	US-09-678-202A-4	Sequence 4, Appli
5	58	100.0	11	US-09-845-726-1	Sequence 1, Appli
6	58	100.0	11	US-10-076-071-4	Sequence 4, Appli
7	58	100.0	11	US-10-186-168-4	Sequence 4, Appli
8	58	100.0	11	US-10-300-664-4	Sequence 4, Appli
9	58	100.0	12	PCT-US00-26952-3	Sequence 3, Appli
10	58	100.0	12	PCT-US00-26952-6	Sequence 6, Appli
11	58	100.0	12	PCT-US02-04275-3	Sequence 3, Appli
12	58	100.0	12	PCT-US02-04275-6	Sequence 6, Appli
13	58	100.0	12	PCT-US02-37136-3	Sequence 3, Appli
14	58	100.0	12	PCT-US02-37136-6	Sequence 6, Appli
15	58	100.0	12	US-09-678-202A-3	Sequence 3, Appli
16	58	100.0	12	US-09-678-202A-6	Sequence 6, Appli
17	58	100.0	12	US-09-846-347-1	Sequence 1, Appli
18	58	100.0	12	US-10-076-071-3	Sequence 3, Appli
19	58	100.0	12	US-10-076-071-6	Sequence 6, Appli
20	58	100.0	12	US-10-186-168-3	Sequence 3, Appli
21	58	100.0	12	US-10-186-168-6	Sequence 6, Appli
22	58	100.0	12	US-10-300-664-3	Sequence 3, Appli
23	58	100.0	12	US-10-300-664-6	Sequence 6, Appli
24	58	100.0	13	PCT-US98-02257-13	Sequence 13, Appli
25	58	100.0	13	US-09-266-768-13	Sequence 13, Appli
26	58	100.0	13	US-09-845-726A-1	Sequence 1, Appli
27	58	100.0	13	US-09-845-764-1	Sequence 1, Appli
28	58	100.0	15	US-09-845-764A-1	Sequence 1, Appli
29	58	100.0	17	US-09-845-727-1	Sequence 1, Appli
30	58	100.0	20	US-08-840-752A-4	Sequence 4, Appli
31	58	100.0	24	US-09-846-328-1	Sequence 1, Appli
32	58	100.0	26	US-09-846-328A-1	Sequence 1, Appli
33	58	100.0	26	US-09-846-329-1	Sequence 1, Appli
34	58	100.0	28	US-09-846-329A-1	Sequence 1, Appli
35	58	100.0	54	1 PCT-US01-08656-10524	Sequence 10524, A
36	58	100.0	69	US-10-424-599-180109	Sequence 180109, A
37	58	100.0	71	US-09-307-590-559	Sequence 559, App
38	58	100.0	71	US-09-307-590-559	Sequence 559, App
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42	58	100.0	76	1 PCT-US02-40892A-674	Sequence 674, App
43	58	100.0	133	1 PCT-US01-08656-5979	Sequence 5979, Ap
44	58	100.0	134	1 PCT-US01-08656-5922	Sequence 5922, Ap
45	58	100.0	144	17 US-09-307-590-612	Sequence 612, App

ALIGNMENTS

RESULT 1
PCT-US00-26952-4
; Sequence 4, Application PC/TUS0026952
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Rao, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3-PCT
; CURRENT APPLICATION NUMBER: PCT/US00/26952
; CURRENT FILING DATE: 2000-09-30
; EARLIER APPLICATION NUMBER: 60/157,404
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 60/211,078
; EARLIER FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-26952-4

Query Match 100.0%; Score 58; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 1 AHKSEVAHRFK 11

RESULT 2
PCT-US02-04275-4
; Sequence 4, Application PC/TUS0204275
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. Gerald
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
; FILE REFERENCE: 4172-3-2-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/04275
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/283,507
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/816,679
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/268,558
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-04275-4

Query Match 100.0%; Score 58; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AHKSEVAHRFK 11

RESULT 3
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; Sequence 4, Application PC/TUS0237136
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ORAL CARE
; FILE REFERENCE: 4172-75-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/37136
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

PCT-US02-37136-4
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Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AHKSEVAHRFK 11

RESULT 4
US-09-678-202A-4
; Sequence 4, Application US/09678202A
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagarajo K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/09/678,202A
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-678-202A-4

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Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 1 AHKSEVAHRFK 11

RESULT 5
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; Sequence 1, Application US/09845726
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
; TITLE OF INVENTION: OF 1424 DALTONS
; FILE REFERENCE: 2132.033
; CURRENT APPLICATION NUMBER: US/09/845,726
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-726-1

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Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AHKSEVAHRFK 11

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; Sequence 4, Application US/10076071
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. Gerald
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
; FILE REFERENCE: 4172-3-2
; CURRENT APPLICATION NUMBER: US/10/076,071
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/283,507
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/816,679
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/268,558
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-071-4

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Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 1 AHKSEVAHRFK 11

RESULT 7
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; Sequence 4, Application US/10186168
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/186,168
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
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; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-168-4

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Best Local Similarity 100.0%; Pred. No. 0.00075;

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Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 1 AHKSEVAHRFK 11

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US-10-300-664-4
; Sequence 4, Application US/10300664
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/300,664
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-664-4

Query Match 100.0%; Score 58; DB 29; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 1 AHKSEVAHRFK 11

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; Sequence 3, Application PC/TUS0026952
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3-PCT
; CURRENT APPLICATION NUMBER: PCT/US00/26952
; CURRENT FILING DATE: 2000-09-30
; EARLIER APPLICATION NUMBER: 60/157,404
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 60/211,078
; EARLIER FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-26952-3

Query Match 100.0%; Score 58; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00075;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
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Db 2 AHKSEVAHREFK 12

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; Sequence 6, Application PC/TUS0026952
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3-PCT
; CURRENT APPLICATION NUMBER: PCT/US00/26952
; CURRENT FILING DATE: 2000-09-30
; EARLIER APPLICATION NUMBER: 60/157,404
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 60/211,078
; EARLIER FILING DATE: 2000-06-13
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
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; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:variant
PCT-US00-26952-6

Query Match 100.0%; Score 58; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
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Db 2 AHKSEVAHREFK 12

RESULT 11
PCT-US02-04275-3
; Sequence 3, Application PC/TUS0204275
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. Gerald
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
; FILE REFERENCE: 4172-3-2-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/04275
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/283,507
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/816,679
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13

; PRIOR APPLICATION NUMBER: 60/268,558
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-04275-3

Query Match 100.0%; Score 58; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
| | | | | | | | | |
Db 2 AHKSEVAHREFK 12

RESULT 12
PCT-US02-04275-6
; Sequence 6, Application PC/TUS0204275
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. Gerald
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
; FILE REFERENCE: 4172-3-2-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/04275
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/283,507
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/816,679
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/268,558
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
PCT-US02-04275-6

Query Match 100.0%; Score 58; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
| | | | | | | | | |
Db 2 AHKSEVAHREFK 12

RESULT 13
PCT-US02-37136-3
; Sequence 3, Application PC/TUS0237136
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David

; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ORAL CARE
; FILE REFERENCE: 4172-75-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/37136
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-37136-3

Query Match 100.0%; Score 58; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |
Db 2 AHKSEVAHRFK 12

RESULT 14

PCT-US02-37136-6
; Sequence 6, Application PC/TUS0237136
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ORAL CARE
; FILE REFERENCE: 4172-75-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/37136
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: ACETYLTATION
PCT-US02-37136-6

Query Match 100.0%; Score 58; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
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Db 2 AHKSEVAHRFK 12

RESULT 15

US-09-678-202A-3
; Sequence 3, Application US/09678202A
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/09/678, 202A
; CURRENT FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-678-202A-3

Query Match 100.0%; Score 58; DB 20; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
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Db 2 AHKSEVAHRFK 12

Search completed: August 29, 2003, 14:37:29
Job time : 439 secs

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OM protein - protein search, using sw model

Run on: August 29, 2003, 14:28:50 ; Search time 56 Seconds
(without alignments)
26.868 Million cell updates/sec

Title: US-09-845-726A-1_COPY_2_12
Perfect score: 58
Sequence: 1 AHKSEVAHRFK 11

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Gapop 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues

Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	11	10	US-09-845-726-1
2	58	100.0	11	12	US-10-300-664-4
3	58	100.0	11	15	US-10-076-071-4
4	58	100.0	11	16	US-10-186-168-4
5	58	100.0	12	11	US-09-846-347-1
6	58	100.0	12	12	US-10-300-664-3
7	58	100.0	12	12	US-10-300-664-6
8	58	100.0	12	15	US-10-076-071-3
9	58	100.0	12	15	US-10-076-071-6
10	58	100.0	12	16	US-10-186-168-3
11	58	100.0	12	16	US-10-186-168-6
12	58	100.0	13	10	US-09-845-764-1
13	58	100.0	17	10	US-09-845-727-1
14	58	100.0	24	10	US-09-846-328-1
15	58	100.0	26	10	US-09-846-329-1

16	58	100.0	195	14	US-10-074-956-24	Sequence 24, Appl
17	58	100.0	241	14	US-10-074-956-27	Sequence 27, Appl
18	58	100.0	268	14	US-10-074-956-28	Sequence 28, Appl
19	58	100.0	585	11	US-09-929-552-2	Sequence 2, Appl
20	58	100.0	585	11	US-09-932-613-445	Sequence 445, Appl
21	58	100.0	585	11	US-09-984-010-26	Sequence 26, Appl
22	58	100.0	585	11	US-09-833-041-18	Sequence 18, Appl
23	58	100.0	585	12	US-10-153-604A-5	Sequence 5, Appl
24	58	100.0	585	14	US-10-153-064-5	Sequence 5, Appl
25	58	100.0	604	11	US-09-984-010-7	Sequence 7, Appl
26	58	100.0	609	11	US-09-919-039-370	Sequence 370, Appl
27	58	100.0	609	12	US-10-153-604A-7	Sequence 7, Appl
28	58	100.0	609	14	US-10-153-064-7	Sequence 7, Appl
29	58	100.0	610	10	US-09-984-186-2	Sequence 2, Appl
30	58	100.0	610	15	US-10-237-667-2	Sequence 2, Appl
31	58	100.0	610	15	US-10-237-708-2	Sequence 2, Appl
32	58	100.0	610	15	US-10-237-866-2	Sequence 2, Appl
33	58	100.0	610	15	US-10-237-871-2	Sequence 2, Appl
34	58	100.0	610	15	US-10-237-624-2	Sequence 2, Appl
35	58	100.0	651	12	US-10-153-604A-133	Sequence 133, App
36	58	100.0	651	14	US-10-153-064-133	Sequence 133, App
37	58	100.0	652	12	US-10-153-604A-96	Sequence 96, Appl
38	58	100.0	652	12	US-10-153-604A-99	Sequence 99, Appl
39	58	100.0	652	12	US-10-153-604A-105	Sequence 105, App
40	58	100.0	652	12	US-10-153-604A-132	Sequence 132, App
41	58	100.0	652	14	US-10-153-064-96	Sequence 96, Appl
42	58	100.0	652	14	US-10-153-064-99	Sequence 99, Appl
43	58	100.0	652	14	US-10-153-064-105	Sequence 105, App
44	58	100.0	652	14	US-10-153-064-132	Sequence 132, App
45	58	100.0	653	12	US-10-153-604A-131	Sequence 131, App

ALIGNMENTS

RESULT 1
US-09-845-726-1
; Sequence 1, Application US/09845726
; Patent No. US20020160417A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
; FILE REFERENCE: 2132, 033
; CURRENT APPLICATION NUMBER: US/09/845,726
; CURRENT FILING DATE: 2000-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-726-1

Query Match 100.0%; Score 58; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 11; /Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
Db 1 AHKSEVAHRFK 11

RESULT 2
US-10-300-664-4
; Sequence 4, Application US/10300664
; Publication No. US2003015811A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.

; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/300,664
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-664-4

Query Match 100.0%; Score 58; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
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Db 1 AHKSEVAHREFK 11
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RESULT 3
US-10-076-071-4
; Sequence 4, Application US/10076071
; Publication No. US20030060408A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. Gerald
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
; FILE REFERENCE: 4172-3-2
; CURRENT APPLICATION NUMBER: US/10/076,071
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/283,507
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/816,679
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/268,558
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-071-4

Query Match 100.0%; Score 58; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
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Db 1 AHKSEVAHREFK 11
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RESULT 4
US-10-186-168-4
; Sequence 4, Application US/10186168
; Publication No. US20030130185A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagarajo K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/186,168
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-168-4

Query Match 100.0%; Score 58; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
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Db 1 AHKSEVAHREFK 11
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RESULT 5
US-09-846-347-1
; Sequence 1, Application US/09846347
; Publication No. US20030040602A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
; FILE REFERENCE: 2132.032
; CURRENT APPLICATION NUMBER: US/09/846,347
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-347-1

Query Match 100.0%; Score 58; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
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Db 2 AHKSEVAHREFK 12
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RESULT 6
US-10-300-664-3
; Sequence 3, Application US/10300664
; Publication No. US2003015811A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David

APPLICANT: Curtis, C. G.
APPLICANT: Lau, Edward
APPLICANT: Rao, Nagaraja K.R.
APPLICANT: Winkler, James V.
APPLICANT: Crook, Wannell M.
TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
FILE REFERENCE: 4172-3
CURRENT APPLICATION NUMBER: US/10/300,664
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US/09/678,202
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/157,404
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/211,078
PRIOR FILING DATE: 2000-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-10-300-664-3

Query Match 100.0%; Score 58; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
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RESULT 7
US-10-300-664-6
Sequence 6, Application US/10300664
Publication No. US20030158111A1
GENERAL INFORMATION:
APPLICANT: Bar-Or, David
APPLICANT: Curtis, C. G.
APPLICANT: Lau, Edward
APPLICANT: Rao, Nagaraja K.R.
APPLICANT: Winkler, James V.
APPLICANT: Crook, Wannell M.
TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
FILE REFERENCE: 4172-3
CURRENT APPLICATION NUMBER: US/10/300,664
CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US/09/678,202
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/157,404
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/211,078
PRIOR FILING DATE: 2000-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION
US-10-300-664-6

Query Match 100.0%; Score 58; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
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RESULT 8
US-10-076-071-3
Sequence 3, Application US/10076071
Publication No. US20030060408A1
GENERAL INFORMATION:
APPLICANT: Bar-Or, David
APPLICANT: Curtis, C. Gerald
APPLICANT: Lau, Edward
APPLICANT: Rao, Nagaraja K.R.
APPLICANT: Winkler, James V.
APPLICANT: Crook, Wannell M.
TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
FILE REFERENCE: 4172-3-2
CURRENT APPLICATION NUMBER: US/10/076,071
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 09/678,202
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/283,507
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/816,679
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/157,404
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,404
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/211,078
PRIOR FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: 60/268,558
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-10-076-071-3

Query Match 100.0%; Score 58; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
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RESULT 9
US-10-076-071-6
Sequence 6, Application US/10076071
Publication No. US20030060408A1
GENERAL INFORMATION:
APPLICANT: Bar-Or, David
APPLICANT: Curtis, C. Gerald
APPLICANT: Lau, Edward
APPLICANT: Rao, Nagaraja K.R.
APPLICANT: Winkler, James V.
APPLICANT: Crook, Wannell M.
TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
FILE REFERENCE: 4172-3-2
CURRENT APPLICATION NUMBER: US/10/076,071
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 09/678,202
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/283,507
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/816,679
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/157,404
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,404
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/211,078
PRIOR FILING DATE: 2001-02-13

; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/268,558
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
US-10-076-071-6

Query Match 100.0%; Score 58; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
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RESULT 10
US-10-186-168-3

; Sequence 3, Application US/10186168
; Publication No. US20030130185A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagarajo K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/186,168
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-168-3

Query Match 100.0%; Score 58; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
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RESULT 11
US-10-186-168-6

; Sequence 6, Application US/10186168
; Publication No. US20030130185A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagarajo K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.

; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/186,168
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: ACETYLATION
US-10-186-168-6

Query Match 100.0%; Score 58; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
|||||

RESULT 12

US-09-845-764-1
; Sequence 1, Application US/09845764
; Patent No. US20020160958A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
; FILE REFERENCE: 2132.037
; CURRENT APPLICATION NUMBER: US/09/845,764
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-764-1

Query Match 100.0%; Score 58; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
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RESULT 13

US-09-845-727-1
; Sequence 1, Application US/09845727
; Patent No. US20020160418A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
; FILE REFERENCE: 2132.047
; CURRENT APPLICATION NUMBER: US/09/845,727
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

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; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-727-1

Query Match      100.0%; Score 58; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AHKSEVAHRFK 11
Db      2 AHKSEVAHRFK 12
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RESULT 14
US-09-846-328-1
; Sequence 1, Application US/09846328
; Patent No. US20020160531A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; FILE REFERENCE: 2132.051
; CURRENT APPLICATION NUMBER: US/09/846,328
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-328-1

Query Match      100.0%; Score 58; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AHKSEVAHRFK 11
Db      2 AHKSEVAHRFK 12
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RESULT 15
US-09-846-329-1
; Sequence 1, Application US/09846329
; Patent No. US20020161177A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: Biopolymer Marker Indicative of Disease State Having A Molecular
; FILE REFERENCE: 2132.052
; CURRENT APPLICATION NUMBER: US/09/846,329
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-329-1

Query Match      100.0%; Score 58; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AHKSEVAHRFK 11
Db      2 AHKSEVAHRFK 12
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Search completed: August 29, 2003, 14:39:04
Job time : 56 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 29, 2003, 14:25:40 ; Search time 29 Seconds
(without alignments)
16.049 Million cell updates/sec

Title: us-09-845-726a-1_COPY_2_12
Perfect score: 58
Sequence: 1 AHKSEVAHRFK 11

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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2.6/prodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	58	100.0	13	2	US-09-024-198-13
3	58	100.0	13	2	US-09-186-409-13
4	58	100.0	585	1	US-08-153-799-14
5	58	100.0	585	1	US-08-448-196A-3
6	58	100.0	585	2	US-08-984-176-1
7	58	100.0	585	2	US-08-702-572-2
8	58	100.0	585	3	US-08-769-746-2
9	58	100.0	609	1	US-08-222-619-3
10	58	100.0	609	1	US-08-433-037-4
11	58	100.0	609	4	US-08-897-956A-2
12	58	100.0	609	5	PCT-US95-04075-3
13	58	100.0	610	2	US-08-797-689-2
14	58	100.0	783	1	US-08-256-938-2
15	58	100.0	787	1	US-08-256-938-4
16	58	100.0	787	2	US-08-797-689-16
17	58	100.0	978	4	US-08-897-956A-3
18	57	98.3	584	1	US-08-448-196A-7
19	53	91.4	582	1	US-08-134-638-1
20	53	91.4	583	1	US-08-448-196A-4
21	50	86.2	13	2	US-08-803-364-6
22	50	86.2	13	2	US-09-024-198-12
23	50	86.2	13	2	US-09-186-409-12
24	50	86.2	16	2	US-08-803-364-1
25	50	86.2	16	2	US-09-024-198-10
26	50	86.2	16	2	US-09-186-409-10
27	48	82.8	583	1	US-08-448-196A-5

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Sequence 7, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 5307, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4377, Ap
Sequence 28283, A
Sequence 27825, A
Sequence 28, Appl
Sequence 73, Appl
Sequence 11, Appl
Sequence 196, App

ALIGNMENTS

RESULT 1
US-08-803-364-7
; Sequence 7, Application US/08803364
; Patent No. 5864014
; GENERAL INFORMATION:
; APPLICANT: FASANO, Alessio
; TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,364
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/_____
; FILING DATE: 20 FEB 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: A-6888
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
US-08-803-364-7

Query Match 100.0%; Score 58; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
|||||||

Db 1 AHKSEVAHREFK 11

RESULT 2

US-09-024-198-13
; Sequence 13, Application US/09024198
; Patent No. 5912323
; GENERAL INFORMATION:
; APPLICANT: FASANO, Alessio
; TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,198
; FILING DATE: 17 FEB 1998

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,364
; FILING DATE: 20 FEB 1997

ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon

REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: A-6988
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860

INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid

TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-09-024-198-13

Query Match 100.0%; Score 58; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11

Db 1 AHKSEVAHREFK 11

RESULT 3

US-09-186-409-13
; Sequence 13, Application US/09186409
; Patent No. 5948629
; GENERAL INFORMATION:
; APPLICANT: FASANO, Alessio

; TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/186,409
; FILING DATE: 5 NOV 1998

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/024,198
; FILING DATE: 17 FEB 1998

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,364
; FILING DATE: 20 FEB 1997

CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon

REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: A-7306
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860

INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid

TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-09-186-409-13

Query Match 100.0%; Score 58; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11

Db 1 AHKSEVAHREFK 11

RESULT 4

US-08-153-799-14
; Sequence 14, Application US/08153799
; Patent No. 5766883
; GENERAL INFORMATION:
; APPLICANT: Ballance, David J

; APPLICANT: Goodey, Andrew R
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: R Hain Swope, BOC Health Care Inc

; STREET: 100 Mountain Avenue
; CITY: Murray Hill
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07974

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,799
; FILING DATE:

CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847975
; FILING DATE: 06-MAR-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8909916.2
; FILING DATE: 29-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB90/00650

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; FILING DATE: 26-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/775952
; FILING DATE: 29-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Swope, R. Hain
; REGISTRATION NUMBER: 24864
; REFERENCE/DOCKET NUMBER: 92H832
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 665 2400
; TELEFAX: (908) 771 6159
; TELEX: 219484
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Region
; LOCATION: 369..419
; OTHER INFORMATION: /note= "Alternative C-termini of
; OTHER INFORMATION: HSA(1-n)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..585
; OTHER INFORMATION: /note= "Amino acid sequence of
; OTHER INFORMATION: natural HSA"
;
US-08-153-799-14

Query Match 100.0%; Score 58; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
|||||

RESULT 5
US-08-448-196A-3
; Sequence 3, Application US/08448196A
; Patent No. 5780594
; GENERAL INFORMATION:
; APPLICANT: CARTER, DANIEL C.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
; TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
; TITLE OF INVENTION: RELATED PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NASA
; STREET: MARSHALL SPACE FLIGHT CENTER
; CITY: HUNTSVILLE
; STATE: ALABAMA
; COUNTRY: USA
; ZIP: 35812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,196A
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BROAD JR., ROBERT L.
; REGISTRATION NUMBER: 18,757
; REFERENCE/DOCKET NUMBER: XX/WFS-28402-2
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: 205-544-0021
; TELEFAX: 205-544-0258
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
;
US-08-448-196A-3

Query Match 100.0%; Score 58; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
|||||

RESULT 6
US-08-984-176-1
; Sequence 1, Application US/08984176
; Patent No. 5948609
; GENERAL INFORMATION:
; APPLICANT: CARTER, DANIEL C
; APPLICANT: HO, JOSEPH X
; APPLICANT: RUKER, FLORIAN
; TITLE OF INVENTION: OXYGEN-TRANSPORTING ALBUMIN-BASED BLOOD REPLACEMENT
; TITLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER
; FILE REFERENCE: 08/984,176
; CURRENT APPLICATION NUMBER: US/08/984,176
; CURRENT FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-08-984-176-1

Query Match 100.0%; Score 58; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
|||||

RESULT 7
US-08-702-572-2
; Sequence 2, Application US/08702572
; Patent No. 5965386
; GENERAL INFORMATION:
; APPLICANT: Kerry-Williams, Sean M
; APPLICANT: Gilbert, Sarah C
; TITLE OF INVENTION: Yeast Strains and Modified Albumins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Centeon L.L.C.
; STREET: 1020 First Avenue
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 6.0
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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/702.572
;; FILING DATE: 11-NOV-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO 95/23857
;; FILING DATE: 1-MAR-1995
;; APPLICATION NUMBER: GB 9404270.2
;; FILING DATE: 5-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Naomi Biswas
;; REGISTRATION NUMBER: 38,384
;; REFERENCE/DOCKET NUMBER: CE0114 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610/878/4294
;; TELEFAX: 610/878/4221
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 585 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-08-702-572-2

Query Match 100.0%; Score 58; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12

RESULT 8
US-08-769-746-2
; Sequence 2, Application US/08769746
; Patent No. 6274305
; GENERAL INFORMATION:
; APPLICANT: Sonnenschein, Carlos
; APPLICANT: Soto, Ana M.
; TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,746
; FILING DATE: 19-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: MBRI-02584
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-769-746-2

Query Match 100.0%; Score 58; DB 3; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12

RESULT 9
US-08-222-619-3
; Sequence 3, Application US/08222619
; Patent No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,619
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-222-619-3

Query Match 100.0%; Score 58; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 26 AHKSEVAHRFK 36

RESULT 10
US-08-433-037-4
; Sequence 4, Application US/08433037
; Patent No. 5707828
; GENERAL INFORMATION:
; APPLICANT: Sreekrishna, Kotikanyadan
; APPLICANT: Barr, Kathryn A.
; APPLICANT: Brerley, Russell A.
; APPLICANT: Thill, Gregory P.
; APPLICANT: Tschopp, Juerg F.
; TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York

; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,037
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 91082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US-897-956A-2

Query Match 100.0%; Score 58; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |
DB 26 AHKSEVAHRFK 36

RESULT 11

US-08-897-956A-2
; Sequence 2, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-08-897-956A-2

Query Match 100.0%; Score 58; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |
DB 26 AHKSEVAHRFK 36

RESULT 12

PCT-US95-04075-3
; Sequence 3, Application PC/TUS9504075
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like

; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04075
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; PCT-US95-04075-3

Query Match 100.0%; Score 58; DB 5; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |
DB 26 AHKSEVAHRFK 36

RESULT 13

US-08-797-689-2
; Sequence 2, Application US/08797689
; Patent No. 5876969
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Fournier, Alain
; APPLICANT: Guitton, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00085

; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38 619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3808
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-797-689-2

Query Match 100.0%; Score 58; DB 2; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
Db 26 AHKSEVAHREFK 36

RESULT 14
US-08-256-938-2
; Sequence 2, Application US/08256938
; Patent No. 5665863
; GENERAL INFORMATION:
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
; TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,938
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/01065
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: ST92007-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 787 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-256-938-4

Query Match 100.0%; Score 58; DB 1; Length 783;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
Db 204 AHKSEVAHREFK 214

Search completed: August 29, 2003, 14:30:04
Job time : 30 secs

QY 1 AHKSEVAHREFK 11
Db 26 AHKSEVAHREFK 36

RESULT 15

US-08-256-938-4
; Sequence 4, Application US/08256938
; Patent No. 5665863
; GENERAL INFORMATION:
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
; TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,938
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/01065
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: ST92007-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 787 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-256-938-4

Query Match 100.0%; Score 58; DB 1; Length 787;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
Db 204 AHKSEVAHREFK 214

Search completed: August 29, 2003, 14:30:04
Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 14:13:44 ; Search time 82 Seconds
(without alignments)
21.293 Million cell updates/sec

Title: US-09-845-726A-1_COPY_2_12
Perfect score: 58
Sequence: 1 AHKSEVAHRFK 11

Scoring table:
BLOSUM62
Gapex 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	58	100.0	11	22	ABG74368
2	58	100.0	11	23	AAE14802
3	58	100.0	11	24	ABG75656
4	58	100.0	12	22	ABG74367
5	58	100.0	12	22	AAE14801
6	58	100.0	12	23	AAE14802
7	58	100.0	12	23	AAE14803
8	58	100.0	12	24	ABG75657
9	58	100.0	13	19	AAW74538

10	58	100.0	13	24	ABG75657	Congestive heart f
11	58	100.0	20	21	AAE12462	Human albumin epit
12	58	100.0	26	24	ABG75942	Human serum albumi
13	58	100.0	28	24	ABU09223	Serum albumin insu
14	58	100.0	113	22	AAO11631	Human polypeptide
15	58	100.0	116	22	AAO02642	Human polypeptide
16	58	100.0	119	22	AAO11632	Human polypeptide
17	58	100.0	123	22	AAO04424	Human polypeptide
18	58	100.0	124	22	AAO02630	Human polypeptide
19	58	100.0	133	4	AAO30004	Sequence encoded b
20	58	100.0	133	22	AAU29925	Novel human secret
21	58	100.0	137	22	AAO12088	Human polypeptide
22	58	100.0	192	22	AAU29875	Novel human secret
23	58	100.0	195	23	AAO17048	Human serum albumi
24	58	100.0	204	21	AAV83947	Yeast codon-biased
25	58	100.0	214	22	AAU29874	Novel human secret
26	58	100.0	236	23	AAO17051	Human albumin-thro
27	58	100.0	241	23	AAO16984	Alpha-MSH construc
28	58	100.0	242	23	AAO16985	Alpha-MSH construc
29	58	100.0	244	23	AAO16986	Alpha-MSH construc
30	58	100.0	245	23	AAO16987	Alpha-MSH construc
31	58	100.0	245	23	AAO16988	Alpha-MSH construc
32	58	100.0	268	23	AAO16989	Alpha-MSH construc
33	58	100.0	289	22	AAU29575	Novel human secret
34	58	100.0	289	22	AAU29581	Novel human secret
35	58	100.0	303	12	AAO14178	Human serum albumi
36	58	100.0	373	10	AAO90387	N-terminal of huma
37	58	100.0	388	10	AAO90389	N-terminal human s
38	58	100.0	389	10	AAO90390	N-terminal human s
39	58	100.0	390	10	AAO90391	N-terminal human s
40	58	100.0	401	22	AAU29876	Novel human secret
41	58	100.0	407	10	AAO90392	N-terminal human s
42	58	100.0	550	22	AAU29877	Novel human secret
43	58	100.0	584	24	ABG72381	Mature human serum
44	58	100.0	585	10	AAO93344	Sequence of mature
45	58	100.0	585	10	AAO90388	Mature human serum

ALIGNMENTS

RESULT 1
AAB74368
ID AAB74368 standard; peptide; 11 AA.
XX AC AAB74368;
XX DT 02-JUL-2001 (first entry)
XX DE Reactive oxygen species inhibitory peptide #4.
XX DE ROS; reactive oxygen species; metal binding; ischemia;
XX DE neurodegenerative.
XX OS Synthetic.
XX OS WO200125765-A1.
XX PD 12-APR-2001.
XX PF 29-SEP-2000; 2000WO-US26952.
XX PR 01-OCT-1999; 99US-0157404.
XX PR 13-JUN-2000; 2000US-0211078.
XX PA (BARC/) BAR-OR D.
XX PA (CURT/) CURTIS C G.
XX PA (LAUE/) LAU E.
XX PA (RAON/) RAO N K R.
XX PA (WINK/) WINKLER J V.
XX PA (CROO/) CROOK W M.
XX PI Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;

102 a) ✓

XX DR WPI; 2001-328322/34.

XX PT Metal binding peptide compounds prevent damage by reactive oxygen

XX PT species in animal organs and tissues, useful for reperfusion,

XX PT transplantation and treating e.g. ischemia, neurological and

XX PT cardiovascular diseases

XX PS Example 10; Page 43; 124pp; English.

XX CC The present invention relates to metal binding peptides that prevent

XX CC damage by reactive oxygen. The peptides may be used for reperfusion

XX CC an ischemic tissue or organ with cerebral or cardiovascular ischemia,

XX CC for treating neurological trauma and for neurodegenerative disease.

XX CC The present sequence is a reactive oxygen species inhibitory peptide.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 58; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.2e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11

DB 1 AHKSEVAHRFK 11

RESULT 2

AAE14802

ID AAE14802 standard; peptide; 11 AA.

AC AAE14802;

DT 24-FEB-2003 (first entry)

DE Human reactive oxygen species generation inhibiting peptide #2.

XX KW Reactive oxygen species; ROS; metal-binding peptide; angiogenesis;

XX KW embryo implantation; endometriosis; tumour; hypertrophy; psoriasis;

XX KW connective tissue disease; ocular angiogenic disease; polyposis;

XX KW cardiovascular disease; cerebral vascular disease; immune disorder;

XX KW sepsis; obesity; acidosis; arthritis; asthma; autoimmune disease;

XX KW cancer; cystic fibrosis; diabetes; hepatitis C; infertility;

XX KW inflammation; inflammatory bowel disease; neurological disease;

XX KW multiple sclerosis; pancreatitis; human.

OS Homo sapiens.

XX WO200264620-A2.

PD 22-AUG-2002.

XX 13-FEB-2002; 2002WO-US04275.

XX 13-FEB-2001; 2001US-268558P.

XX 22-MAR-2001; 2001US-0816679.

XX 04-APR-2001; 2001US-281648P.

XX 11-APR-2001; 2001US-283507P.

XX (DMTB-) DMI BIOSCIENCES INC.

XX Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;

XX WPI; 2002-691590/74.

XX New method for the inhibition of angiogenesis and the treatment of

XX angiogenic disease, sepsis, and a disease involving acidosis, comprises

XX the administration of a specified peptide or its salt -

XX Example 10; Page 56; 129pp; English.

XX The invention relates to a method for reducing molecular, cellular

XX and tissue damage done by reactive oxygen species (ROS) and also

XX

reducing concentration of a metal ion in an animal using specific

metal-binding peptides and their derivatives that bind metal ions.

The compounds of the invention are useful for inhibiting angiogenesis

(including required for embryo implantation e.g. in endometriosis), and

for treating angiogenic diseases, such as tumour (preferably a benign

tumour), tumour metastasis, hypertrophy, connective tissue disorder,

psoriasis, ocular angiogenic disease, cardiovascular disease, cerebral

vascular disease, polyposis, obesity, immune disorder, sepsis, and a

disease or condition involving acidosis. The compounds are also useful in

the treatment of ARDS, aging, AIDS, arteriosclerosis (hypertension,

senility and impotence), arthritis, asthma, autoimmune diseases,

cancer, chronic granulomatous disease, cirrhosis, colitis, Crohn's

disease, cystic fibrosis, (neuro)degenerative diseases, diabetes

(diabetic retinopathy, renal disease, impotence and peripheral vascular

disease), eye diseases, emphysema, head and traumatic brain injury,

hepatitis C, infertility, inflammation, inflammatory bowel disease,

metastasis, ischaemia, neoplastic diseases, neurological diseases,

multiple sclerosis, pancreatitis, peripheral vascular disease, prion

disease, pulmonary embolism, reperfusion, scleroderma, sepsis, shock,

tissue damage, toxic reactions (e.g. poisoning (herbicide, transition

metal, carbon monoxide, and antibiotic toxicity). The present

sequence is a human peptide that inhibits generation of reactive

oxygen species (ROS).

Sequence 11 AA;

Query Match 100.0%; Score 58; DB 23; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.2e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11

DB 1 AHKSEVAHRFK 11

RESULT 3

ABG75656

ID ABG75656 standard; Peptide; 11 AA.

AC ABG75656;

DT 13-MAY-2003 (first entry)

DE Congestive heart failure disease specific marker #1.

XX KW Biopolymer marker; serum albumin; disease specific marker;

XX KW congestive heart failure.

XX Unidentified.

OS US2002160417-A1.

PN 31-OCT-2002.

XX 30-APR-2001; 2001US-0845726.

XX 30-APR-2001; 2001US-0845726.

XX (JACK/) JACKOWSKI G.

XX (STAN/) STANTON EB.

XX (THAT/) THATCHER B.

XX (VREE/) VREES T.

XX (YANT/) YANTHA J.

XX (MARS/) MARSHALL J.

XX Jackowski G, Stanton EB, Thatcher B, Vrees T, Yantha J;

XX Marshall J;

XX WPI; 2003-246641/25.

XX Novel biopolymer marker such as serum albumin having specific molecular

XX weight, useful in indicating disease state such as congestive heart

XX failure -

XX Claim 1; Page 7; 10pp; English.
PS The invention relates to a biopolymer marker such as serum albumin having
CC a molecular weight of about 1424 daltons, useful in indicating at least
CC one particular disease state. The biopolymer marker is useful for
CC indicating at least one particular disease state such as congestive heart
CC failure and as an antigen in immunoassays for the detection of those
CC individuals suffering from the disease known to be evidenced by the
CC marker sequence. The biopolymer marker rapidly and accurately diagnoses a
CC disease state such as congestive heart failure and allows physicians to
CC identify asymptomatic patients before they develop the disease state.
CC This sequence represents a congestive heart failure disease specific
CC marker.

XX SQ Sequence 11 AA;
Query Match 100.0%; Score 58; DB 24; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |
Db 1 AHKSEVAHRFK 11

RESULT 4
AAB74367
ID AAB74367 standard; peptide; 12 AA.
AC AAB74367;
XX 02-JUL-2001 (first entry)
DT Reactive oxygen species inhibitory peptide #3.

DE ROS; reactive oxygen species; metal binding; ischemia;
KW neurodegenerative.

XX Synthetic.

XX WO200125265-A1.

XX 12-APR-2001.

XX 29-SEP-2000; 2000WO-US26952.

XX 01-OCT-1999; 99US-0157404.

XX 13-JUN-2000; 2000US-0211078.

XX (BARO/) BAR-OR D.

XX (CURT/) CURTIS C G.

XX (LAUE/) LAU E.

XX (RAON/) RAO N K R.

XX (WINK/) WINKLER J V.

XX (CROO/) CROOK W M.

XX Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;
WPI; 2001-328322/34.

XX Metal binding peptide compounds prevent damage by reactive oxygen
species in animal organs and tissues, useful for reperfusion,
transplantation and treating e.g. ischemia, neurological and
cardiovascular diseases

XX Example 10; Page 43; 124pp; English.

XX The present invention relates to metal binding peptides that prevent
CC damage by reactive oxygen. The peptides may be used for reperfusion
CC an ischemic tissue or organ with cerebral or cardiovascular ischemia,
CC for treating neurological trauma and for neurodegenerative disease.
CC The present sequence is a reactive oxygen species inhibitory peptide.

XX SQ Sequence 12 AA;
Query Match 100.0%; Score 58; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |
Db 2 AHKSEVAHRFK 12

RESULT 5
AAB74370
ID AAB74370 standard; peptide; 12 AA.

XX AAB74370;

XX 02-JUL-2001 (first entry)

DE Reactive oxygen species inhibitory peptide #6.

XX ROS; reactive oxygen species; metal binding; ischemia;
KW neurodegenerative.

XX Synthetic.

XX WO200125265-A1.

XX 12-APR-2001.

XX 29-SEP-2000; 2000WO-US26952.

XX 01-OCT-1999; 99US-0157404.

XX 13-JUN-2000; 2000US-0211078.

XX (BARO/) BAR-OR D.

XX (CURT/) CURTIS C G.

XX (LAUE/) LAU E.

XX (RAON/) RAO N K R.

XX (WINK/) WINKLER J V.

XX (CROO/) CROOK W M.

XX Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;
WPI; 2001-328322/34.

XX Metal binding peptide compounds prevent damage by reactive oxygen
species in animal organs and tissues, useful for reperfusion,
transplantation and treating e.g. ischemia, neurological and
cardiovascular diseases

XX Example 10; Page 43; 124pp; English.

XX The present invention relates to metal binding peptides that prevent
CC damage by reactive oxygen. The peptides may be used for reperfusion
CC an ischemic tissue or organ with cerebral or cardiovascular ischemia,
CC for treating neurological trauma and for neurodegenerative disease.
CC The present sequence is a reactive oxygen species inhibitory peptide.

XX SQ Sequence 12 AA;
Query Match 100.0%; Score 58; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |
Db 2 AHKSEVAHRFK 12

RESULT 6
AAB14801

AAE14801 standard; peptide; 12 AA.
AAE14801;
24-FEB-2003 (first entry)
Human reactive oxygen species generation inhibiting peptide #1.
Reactive oxygen species; ROS; metal-binding peptide; angiogenesis;
embryo implantation; endometriosis; tumour; hypertrophy; psoriasis;
connective tissue disorder; ocular angiogenic disease; polyposis;
cardiovascular disease; cerebral vascular disease; immune disorder;
sepsis; obesity; acidosis; arthritis; asthma; autoimmune disease;
cancer; cystic fibrosis; diabetes; hepatitis C; infertility;
inflammation; inflammatory bowel disease; neurologic disease;
multiple sclerosis; pancreatitis; human.
Homo sapiens.
WO200264620-A2.
22-AUG-2002.
13-FEB-2002; 2002WO-US04275.
13-FEB-2001; 2001US-268558P.
22-MAR-2001; 2001US-0816679.
04-APR-2001; 2001US-281648P.
11-APR-2001; 2001US-283507P.
(DMTB-) DMI BIOSCIENCES INC.
Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;
WPI; 2002-691590/74.
New method for the inhibition of angiogenesis and the treatment of
angiogenic disease, sepsis, and a disease involving acidosis, comprises
the administration of a specified peptide or its salt -
Example 10; Page 56; 129pp; English.
The invention relates to a method for reducing molecular, cellular
and tissue damage done by reactive oxygen species (ROS) and also
reducing concentration of a metal ion in an animal using specific
metal-binding peptides and their derivatives that bind metal ions.
The compounds of the invention are useful for inhibiting angiogenesis
(including required for embryo implantation e.g. in endometriosis), and
for treating angiogenic diseases such as tumour (preferably a benign
tumour), tumour metastasis, hypertrophy, connective tissue disorder,
psoriasis, ocular angiogenic disease, cardiovascular disease, cerebral
vascular disease, polyposis, obesity, immune disorder, sepsis, and a
disease or condition involving acidosis. The compounds are also useful in
the treatment of ARDS, aging, AIDS, arteriosclerosis (hypertension,
senility and impotence), arthritis, asthma, autoimmune diseases,
cancer, chronic granulomatous disease, cirrhosis, colitis, Crohn's
disease, cystic fibrosis, (neuro)degenerative diseases, diabetes
(diabetic retinopathy, renal disease, impotence and peripheral vascular
disease), eye diseases, emphysema, head and traumatic brain injury,
hepatitis C, infertility, inflammation, inflammatory bowel disease,
metastasis, ischaemia, neoplastic diseases, neurological diseases,
multiple sclerosis, pancreatitis, peripheral vascular disease, prion
disease, pulmonary embolism, reperfusion, scleroderma, sepsis, shock,
tissue damage, toxic reactions (e.g. poisoning (herbicide, transition
metal, carbon monoxide, and antibiotic toxicity). The present
sequence is a human peptide that inhibits generation of reactive
oxygen species (ROS).
Sequence 12 AA;
Query Match 100.0%; Score 58; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |
Db 2 AHKSEVAHRFK 12
RESULT 7
AAE14804
ID AAE14804 standard; peptide; 12 AA.
XX
AC AAE14804;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human reactive oxygen species generation inhibiting peptide #4.
XX
KW Reactive oxygen species; ROS; metal-binding peptide; angiogenesis;
embryo implantation; endometriosis; tumour; hypertrophy; psoriasis;
connective tissue disorder; ocular angiogenic disease; polyposis;
cardiovascular disease; cerebral vascular disease; immune disorder;
sepsis; obesity; acidosis; arthritis; asthma; autoimmune disease;
cancer; cystic fibrosis; diabetes; hepatitis C; infertility;
inflammation; inflammatory bowel disease; neurologic disease;
multiple sclerosis; pancreatitis; human.
XX
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetylated"
FT
XX WO200264620-A2.
XX 22-AUG-2002.
XX
XX 13-FEB-2002; 2002WO-US04275.
XX
XX 13-FEB-2001; 2001US-268558P.
PR 22-MAR-2001; 2001US-0816679.
PR 04-APR-2001; 2001US-281648P.
PR 11-APR-2001; 2001US-283507P.
XX
XX (DMTB-) DMI BIOSCIENCES INC.
XX
XX Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;
WPI; 2002-691590/74.
XX
XX New method for the inhibition of angiogenesis and the treatment of
angiogenic disease, sepsis, and a disease involving acidosis, comprises
the administration of a specified peptide or its salt -
Example 10; Page 57; 129pp; English.
The invention relates to a method for reducing molecular, cellular
and tissue damage done by reactive oxygen species (ROS) and also
reducing concentration of a metal ion in an animal using specific
metal-binding peptides and their derivatives that bind metal ions.
The compounds of the invention are useful for inhibiting angiogenesis
(including required for embryo implantation e.g. in endometriosis), and
for treating angiogenic diseases such as tumour (preferably a benign
tumour), tumour metastasis, hypertrophy, connective tissue disorder,
psoriasis, ocular angiogenic disease, cardiovascular disease, cerebral
vascular disease, polyposis, obesity, immune disorder, sepsis, and a
disease or condition involving acidosis. The compounds are also useful in
the treatment of ARDS, aging, AIDS, arteriosclerosis (hypertension,
senility and impotence), arthritis, asthma, autoimmune diseases,
cancer, chronic granulomatous disease, cirrhosis, colitis, Crohn's
disease, cystic fibrosis, (neuro)degenerative diseases, diabetes
(diabetic retinopathy, renal disease, impotence and peripheral vascular
disease), eye diseases, emphysema, head and traumatic brain injury,
hepatitis C, infertility, inflammation, inflammatory bowel disease,
metastasis, ischaemia, neoplastic diseases, neurological diseases,
multiple sclerosis, pancreatitis, peripheral vascular disease, prion
disease, pulmonary embolism, reperfusion, scleroderma, sepsis, shock,
tissue damage, toxic reactions (e.g. poisoning (herbicide, transition
metal, carbon monoxide, and antibiotic toxicity). The present
sequence is a human peptide that inhibits generation of reactive
oxygen species (ROS).

CC metastasis, ischaemia, neoplastic diseases, neurological diseases,
CC multiple sclerosis, pancreatitis, peripheral vascular disease, prion
CC disease, pulmonary embolism, reperfusion, scleroderma, sepsis, shock,
CC tissue damage, toxic reactions (e.g. poisoning (herbicide, transition
CC metal, carbon monoxide, and antibiotic toxicity). The present
CC sequence is a human peptide that inhibits generation of reactive
CC oxygen species (ROS).
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 58; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |
Db 2 AHKSEVAHRFK 12

RESULT 8
ABB99709
ID ABB99709 standard; peptide; 12 AA.

XX ABB99709;

DT 28-MAR-2003 (first entry)

DE Biopolymer marker indicative of congestive heart failure.

XX Biopolymer marker; congestive heart failure.

OS Homo sapiens.

PN WO20028723-A2.

PD 07-NOV-2002.

XX 26-APR-2002; 2002WO-CA00611.

PR 30-APR-2001; 2001US-0846347.

XX (SYNX-) SYN.X PHARMA INC.

PI Jackowski G, Thatcher B, Vrees T, Yantha J, Marshall J;

DR WPI; 2003-111906/10.

XX New biopolymer marker for use in diagnostic assays for the detection or
PT characterization of a particular disease state, especially congestive
PT heart failure

PS Claim 1; Page 28; 28pp; English.

XX The present sequence represents a biopolymer marker which is indicative
CC of congestive heart failure. The biopolymer marker is used for
CC evidencing and categorizing a disease state. It is used in an assay
CC diagnostic kit and in diagnosing, determining risk-assessment, and
CC identifying therapeutic avenues related to a disease state, such as
CC congestive heart failure. Controlling the presence or absence of the
CC biopolymer marker is used to regulate a disease state.

SQ Sequence 12 AA;

Query Match 100.0%; Score 58; DB 24; Length 12;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |
Db 2 AHKSEVAHRFK 12

RESULT 9

AAW74538
ID AAW74538 standard; peptide; 13 AA.

XX AAW74538;

DT 02-DEC-1998 (first entry)

XX Human serum albumin fragment.

XX Human; zonula occludens toxin receptor; ZOT receptor;

KW agonist; antagonist; toxin; anti-inflammatory drug; antibody;

KW gastrointestinal; inflammatory bowel disease; food allergy;

KW protein losing enteropathy; coeliac disease; adsorption enhancer;

XX fusion protein; serum albumin.

OS Homo sapiens.

XX WO9837096-A1.

PN 27-AUG-1998.

XX 18-FEB-1998; 98WO-US02257.

PR 17-FEB-1998; 98US-0024198.

PR 20-FEB-1997; 97US-0803364.

XX (UYMA-) UNIV MARYLAND BALTIMORE.

XX Fasano A;

PI WPI; 1998-467493/40.

XX New zonula occludens toxin receptors - for identifying receptor
PT antagonists which can be used as anti-inflammatory drugs and
PT agonists useful as intestinal/nasal adsorption enhancers

XX Example 7; Page 49; 68pp; English.

XX This is the amino acid sequence of a fragment of the human serum
CC albumin used in the method of the invention where human zonula
CC occludens toxin (ZOT) receptor is used. The ZOT receptor is used
CC as capture ligand in affinity assays for agonists and antagonists
CC of the toxin. Antagonists of ZOT are specifically useful as
CC anti-inflammatory drugs in the treatment of gastrointestinal
CC conditions that display an increased intestinal permeability, e.g.
CC inflammatory bowel diseases, protein losing enteropathy, food
CC allergies, and coeliac disease. Agonists of ZOT can rapidly open
CC tight junctions in a reversible and reproducible manner and are
CC useful as intestinal or nasal adsorption enhancers. The receptors
CC are also useful for generating monoclonal or polyclonal antibodies
CC (using conventional techniques), and to purify ZOT and fusion
CC proteins comprising ZOT by affinity chromatography.

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 58; DB 19; Length 13;

Best Local Similarity 100.0%; Pred. No. 8.7e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |

Db 1 AHKSEVAHRFK 11

RESULT 10

ABG75657

ID ABG75657 standard; Peptide; 13 AA.

XX ABG75657;

DT 13-MAY-2003 (first entry)

DE Congestive heart failure disease specific marker #2.

```

XX Biopolymer marker; serum albumin; disease specific marker;
KW congestive heart failure.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Residue is optionally absent"
FT Misc-difference 13 /note= "Residue is optionally absent"
FT
XX
XX US2002160417-A1.
XX
XX 31-OCT-2002.
XX
XX 30-APR-2001; 2001US-0845726.
XX
XX 30-APR-2001; 2001US-0845726.
XX
XX (JACK/) JACKOWSKI G.
XX (STAN/) STANTON E B.
XX (THAT/) THATCHER B.
XX (VREE/) VREERES T.
XX (YANT/) YANTHA J.
XX (MAR/) MARSHALL J.
XX
XX Jackowski G, Stanton EB, Thatcher B, Vrees T, Yantha J;
XX Marshall J;
XX
XX WPI; 2003-246641/25.
XX
XX Novel biopolymer marker such as serum albumin having specific molecular
XX weight, useful in indicating disease state such as congestive heart
XX failure -
XX
XX Disclosure; Fig 1; 10pp; English.
XX
XX The invention relates to a biopolymer marker such as serum albumin having
XX a molecular weight of about 1424 daltons, useful in indicating at least
XX one particular disease state. The biopolymer marker is useful for
XX indicating at least one particular disease state such as congestive heart
XX failure and as an antigen in immunoassays for the detection of those
XX individuals suffering from the disease known to be evidenced by the
XX marker sequence. The biopolymer marker rapidly and accurately diagnoses a
XX disease state such as congestive heart failure and allows physicians to
XX identify asymptomatic patients before they develop the disease state.
XX This sequence represents a congestive heart failure disease specific
XX marker.
XX
XX Sequence 13 AA;
XX
XX Query Match 100.0%; Score 58; DB 24; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 8.7e-05;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AHKSEVAHRFK 11
XX | | | | | | | | | |
XX Db 2 AHKSEVAHRFK 12
XX
XX RESULT 11
XX AAB12462
XX ID AAB12462 standard; Peptide; 20 AA.
XX
XX AC AAB12462;
XX
XX 25-OCT-2000 (first entry)
XX
XX Human albumin epitope peptide #1.
XX
XX Monoclonal antibody; hybridoma cell; immunoglobulin; IgG; fusion;
XX human albumin; diabetic nephropathy; diagnosis.

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XX Homo sapiens.
XX
XX JP2000139460-A.
XX
XX 23-MAY-2000.
XX
XX 02-NOV-1998; 98JP-0311677.
XX
XX 02-NOV-1998; 98JP-0311677.
XX
XX (TOYW ) TOYOTA CHUO KENKYUSHO KK.
XX (AISE ) AISIN SEIKI KK.
XX
XX WPI; 2000-433935/38.
XX
XX Hybridoma cells for preparation of IgG monoclonal antibody capable of
XX rapid reaction with human albumin for diagnosis of diabetic nephropathy
XX
XX Example; Fig 1; 11pp; Japanese.
XX
XX The present invention describes hybridoma cells used for preparing an
XX immunoglobulin G (IgG) monoclonal antibody capable of rapid reaction
XX with human albumin. The hybridoma cells are prepared by fusion of mamal
XX myeloma cells and spleen cells immunised with human serum albumin, and
XX producing IgG monoclonal antibody which rapidly react with human
XX albumin. The monoclonal antibodies can be used in the diagnosis of
XX diabetic nephropathy. The present sequence represents a human albumin
XX epitope peptide sequence which is used in an example from the present
XX invention.
XX
XX Sequence 20 AA;
XX
XX Query Match 100.0%; Score 58; DB 21; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 0.00014;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AHKSEVAHRFK 11
XX | | | | | | | | | |
XX Db 3 AHKSEVAHRFK 13
XX
XX RESULT 12
XX ABG75942
XX ID ABG75942 standard; peptide; 26 AA.
XX
XX AC ABG75942;
XX
XX 08-MAY-2003 (first entry)
XX
XX Human serum albumin biopolymer marker peptide.
XX
XX Human; serum albumin; biopolymer marker; SELDI;
XX Surface Enhanced Laser Desorption Ionization mass spectrometry;
XX time-of-flight detection procedure; complement system disease;
XX syndrome X; insulin resistance; hyperinsulinaemia.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 1 /note= "Optionally absent"
XX
XX Misc-difference 2..25 /note= "Specifically claimed in claim 1"
XX
XX Misc-difference 26 /note= "Optionally absent"
XX
XX US2002160531-A1.
XX
XX 31-OCT-2002.
XX
XX 30-APR-2001; 2001US-0846328.
XX
XX

```


CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 113 AA;
 Query Match 100.0%; Score 58; DB 22; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
 Db 30 AHKSEVAHREFK 40
 |||||

RESULT 15
 AAO02642
 ID AAO02642 standard; Protein; 116 AA.

XX AC AAO02642;

XX DT 06-NOV-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 16534.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX OS Homo sapiens.

XX PN WO200164835-A2.

XX PD 07-SEP-2001.

XX PF 26-FEB-2001; 2001WO-US04927.

XX PR 28-FEB-2000; 2000US-0515126.

XX PR 18-MAY-2000; 2000US-0577409.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-514838/56.

XX DR N-PSDB; AAI82573.

XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX PS Claim 20; SEQ ID NO 16534; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating

CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 116 AA;

Query Match 100.0%; Score 58; DB 22; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
 Db 23 AHKSEVAHREFK 33
 |||||

Search completed: August 29, 2003, 14:26:28
 Job time : 84 secs